7.0 SEQUENCE LISTING

SEQUENCE LISTING

	0-20	
5	(1) GENI	ERAL INFORMATION:
5	(i)	APPLICANT: Baum, James A.
	(-)	Gilmer, Amy Jelen
		Mettus, Anne-Marie Light
		recous, rance harre signe
10	(ii)	TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
		LEPIDOPTERAN-ACTIVE-δ-ENDOTOXINS
	(iii)	NUMBER OF SEQUENCES: 76
15	(iv)	CORRESPONDENCE ADDRESS:
	,_,,	(A) ADDRESSEE: Arnold, White & Durkee
		(B) STREET: P.O. Box 4433
		(C) CITY: Houston
		(D) STATE: Texas
20□		(E) COUNTRY: USA
١D		(F) ZIP: 77210
*		
25.	(v)	COMPUTER READABLE FORM:
ļ.		(A) MEDIUM TYPE: Floppy disk
25. j		(B) COMPUTER: IBM PC compatible
		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
₹		(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
ļá		
D	(vi)	CURRENT APPLICATION DATA:
30		(A) APPLICATION NUMBER: US Unknown
LA		(B) FILING DATE:
30		(C) CLASSIFICATION: Unknown
<u> </u>		
•	(vii)	PRIOR APPLICATION DATA:
35		(A) APPLICATION NUMBER: US 08/757,536
		(B) FILING DATE: 27-NOV-1996
	(viii)	ATTORNEY/AGENT INFORMATION:
		(A) NAME: Kitchell, Barbara S.
40		(B) REGISTRATION NUMBER: 33,928
		(C) REFERENCE/DOCKET NUMBER: MECO: 206
	(ix)	TELECOMMUNICATION INFORMATION:
	•	(A) TELEPHONE: 512/418-3000
45		(B) TELEFAX: 512/474-7577
		·

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
5 (A) NAME/KEY: CDS
(B) LOCATION: 1..3567

(xi) SEOUENCE DESCRIPTION: SEO ID NO:1:

	(xi) SE	QUEN	ICE D	ESCR	IPTI	ON:	SEQ	ID N	0:1:				
10	Glu				Gln	AAT Asn								48
15				Val		TTG Leu							AAT Asn	96
20 []						CTG Leu								144
0 0 2 5 1						TTT Phe 55								192
adha . N mark						CAA Gln								240
304 CT						ATA Ile								288
35						GGA Gly								336
40						GAT Asp								384
45						ATA Ile 135								432
						GGA Gly								480
50						CAT His								528

				Trp				Ile			Asn	TAT Tyr	576
5						_				 Суз		AAT Asn	624
10	 _			_	TTA Leu						_	GAT Asp	672
15					CGA Arg 230							TTA Leu 240	720
20					TTT Phe								768
***					CTA Leu								816
25	_			_	TTA Leu	_							864
л 3 6 С					GCA Ala								912
353 353				_	TTT Phe 310	_							960
40			Gly		CGA Arg								1008
70		Ser			TAT Tyr		Arg						1056
45					GGA Gly	Pro							1104
50					CAA Gln								1152

		Val			Phe			ACA Thr 395	Asn			TAT Tyr 400	1200
5				Val				GAA Glu				Asp	1248
10								CAT His					1296
15								TTA Leu				GTA Val	1344
20								ACA Thr					1392
								GGA Gly 475					1440
10 7551 4 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1								ACA Thr					1488
17 12 13								CTA Leu					1536
5						-		TTT Phe		 	_		1584
40								GCG Ala					1632
								CAG Gln 555					1680
45	GGG Gly							TAT Tyr					1728
50	CCT Pro							ATT Ile					1776

			Gly				Ser				Tyr		GAT Asp	1824
5		Glu				Asp							GAT Asp	1872
10	Glu									ACT Thr				1920
15								Tyr		ATT Ile			GTA Val	1968
20										CTG Leu				2016
										CTC Leu 685				2064
25 3										AAT Asn				2112
4∏ 3Q }≟										CAA Gln				2160
35 mm			Lys							ACC Thr				2208
40		Pro							-	TCG Ser		TTA Leu		2256
40	Tyr				Leu					GAT Asp 765	_			2304
45										GAA Glu				2352
50				Gly						CAA Gln		Pro		2400

					Pro				Pro			AAT Asn	2448
5		CTA Leu											2496
10		CAT His 835											2544
15		TTA Leu										GGC Gly	2592
20		AGA Arg											2640
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		GCA Ala											2688
25 TU		GAG Glu											2736
30 L G G	AAA Lys	TCT Ser 915				Leu							2784
355	CAA Gln	GAT Asp			Ile .								2832
40		ATC Ile		Glu .					 		 	 	2880
		GCG Ala	Ala					Leu			Phe		2928
45		TTA Leu					Asn						2976
	AAT Asn					Asn				Val	Val		3024

																GAA Glu	307
	-	101			3	501	101					102	-	514		014	
5																CGT	3120
			Gln	Glu	Val	_		Cys	Pro	Gly	_	-	Tyr	Ile	Leu	Arg	
	102	5				103	0				103	5				1040	
10				TAT													3168
10	Val	Tnr	Ala	Tyr	Lys 104		GIY	Tyr	GIY	GIU 105	_	Cys	Val	Thr	11e 105		
	GAG	ATC	GAA	GAC	AAT	ACA	GAC	GAA	CTG	AAA	TTC	AGC	AAC	TGT	GTA	GAA	3216
																Glu	
15				1060			_		1065	-				1070		•	
	GAG	GAA	GTA	TAT	CCA	AAC	AAC	ACA	GTA	ACG	TGT	AAT	AAT	TAT	ACT	GGG	3264
	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 1085	-	Thr	Gly	
20																	
Ō				GAA													3312
	THE	1090		Glu	Tyr	GIU	1095		TYE	Thr	ser	1100		GIN	GIÀ	Tyr	
25	GAC	GAA	GCC	TAT	GGT	ДДТ	AAC	ССТ	TCC	GTA	CCA	GCT	СДТ	TAC	CCT	тса	3360
				Tyr													3300
	1109			•	•	1110					1115					1120	
¥	GTC	TAT	GAA	GAA	AAA	TCG	TAT	ACA	GAT	GGA	CGA	AGA	GAG	AAT	CCT	TGT	3408
30≟	Val	Tyr	Glu	Glu	Lys	Ser	Tyr	Thr	qzA	Gly	Arg	Arg	Glu	Asn	Pro	Cys	
45 cm cm cm 42 cm					1125	,				1130					1135		
I	GAA	TCT	AAC	AGA	GGC	TAT	GGG	GAT	TAC	ACA	CCA	CTA	CCG	GCT	GGT	TAT	3456
Ę	Glu	Ser	Asn	Arg	-	Tyr	Gly	Asp			Pro	Leu				Tyr	
ڇڌِ(1140	•				1145					1150	•		
				GAT													3504
	Val	Thr	_	Asp	Leu	Glu	Tyr			Glu	Thr	Asp	_		Trp	Ile	
10			1155	ì				1160	•				1165				
	GAG	ATC	GGA	GAA	ACA	GAA	GGA	ACA	TTC	ATC	GTG	GAT	AGC	GTG	GAA	TTA	3552
	Glu	Ile	Gly	Glu	Thr	Glu	Gly	Thr	Phe	Ile	Val	Asp	Ser	Val	Glu	Leu	
		1170)				1175					1180)				
15	CTC	CTT	ATG	GAG	GAA												3567
			Met	Glu	Glu												
	1185	;															

50 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5		(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	2:				
	Met 1		Glu	Asn	Asn 5	Gln	Asn	Gln	Cys	Ile 10	Pro	Tyr	Asn	Cys	Leu 15	Ser
10	Asn	Pro	Glu	Glu 20	Val	Leu	Leu	Asp	Gly 25	Glu	Arg	Ile	Ser	Thr 30	Gly	Asn
15	Ser	Ser	Ile 35	Asp	Ile	Ser	Leu	Ser 40	Leu	Val	Gln	Phe	Leu 45	Val	Ser	Asn
	Phe	Vål 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp
20 10	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe 75	Leu	Val	Gln	Ile	Glu 80
25	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile
25.	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala
ŧ	Phe	Lys	Glu 115	Trp	Glu	Glu	Asp	Pro 120	Asn	Asn	Pro	Ala	Thr 125	Arg	Thr	Arg
30 - 30	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile
<u>5</u> 35	Pro 145	Ser	Phe	Ala	Ile	Ser 150	Gly	Phe	Glu	Val	Pro 155	Leu	Leu	Ser	Val	Tyr 160
	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170	Leu	Arg	Asp	Ser	Val 175	Ile
40	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
45	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Cys	Ala	Asn
	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Lys	Ser 220	Thr	Tyr	Gln	Asp
50	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile

	Gln	Pro	Val	Gly 260		Leu	Thr	Arg	Glu 265		Tyr	Thr	Asp	Pro 270		Ile
5	Asn	Phe	Asn 275		Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
	Val	Met 290		Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
10	Asn 305	Asn	Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315	Val	Gly	Arg	Asn	Phe 320
15	Tyr	Trp	Gly	Gly	His 325	Arg	Val	Ile	Ser	Ser 330	Leu	Ile	Gly	Gly	Gly 335	Asn
	Ile	Thr	Ser	Pro 340	Ile	Tyr	Gly	Arg	Glu 345	Ala	Asn	Gln	Glu	Pro 350	Pro	Arg
20	Ser	Phe	Thr 355	Phe	Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365	Asn	Pro	Thr
	Leu	Arg 370	Leu	Leu	Gln	Gln	Pro 375	Trp	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
2 5	Gly 385	Val	Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
√ UN 30	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
ra C	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys 430	His	Ala
ιπ 8 5 0 1≟	Thr	Phe	Val 435	Gln	Arg	Ser	Gly	Thr 440	Pro	Phe	Leu	Thr	Thr 445	Gly	Val	Val
•	Phe	Ser 450	Trp	Thr	His		Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro
10	Glu 465	Arg	Ile	Asn		Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
15	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe 490	Thr	Gly	Gly	Asp	Ile 495	Leu
	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn
50	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe	Arg	Tyr 525	Ala	Ser	Ser
	Arg	Asp	Ala	Arg	Val		Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val

	545	•	, GII	. vai	. ser	550		i Met	. PI) Der	555		int	met	GIU	560
5	Gly	/ Glu	Asn	. Leu	Thr 565		Arg	Thr	Phe	Arg 570		Thr	Asp	Phe	Ser 575	
	Pro	Phe	Ser	Phe 580		Ala	Asn	Pro	Asp 585	Ile	Ile	Gly	Ile	Ser 590		Glr
10	Pro	Leu	Phe 595		Ala	Gly	Ser	Ile 600	Ser	Ser	Gly	Glu	Leu 605	Tyr	Ile	Asp
15	Lys	Ile 610		Ile	Ile	Leu	Ala 615	Asp	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp
.,	Leu 625		Arg	Ala	Gln	Lys 630	Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
20	Gln	Ile	Gly	Leu	Lys 645	Thr	Asp	Val	Thr	Asp 650	Tyr	His	Ile	Asp	Gln 655	Val
	Ser	Asn	Leu	Val 660	Asp	Cys	Leu	Ser	Asp 665	Glu	Phe	Cys	Leu	Asp 670	Glu	Lys
25.i	Arg	Glu	Leu 675	Ser	Glu	Lys	Val	Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
30	Arg	Asn 690	Leu	Leu	Gln	Asp	Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
 -	Asp 705	Arg	Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	Asp 720
35	Asp	Val	Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp 735	Glu
-	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745	Ile	Asp	Glu	Ser	Lys 750	Leu	Lys
40	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	A rg 760	Gly	Tyr	Ile	Glu	Asp 765	Ser	Gln	Asp
45	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn
	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800
50	Gly	Lys	Суз	Gly	Glu 805	Pro	Asn	Arg	Cys	Ala 810	Pro	His	Leu	Glu	Trp 815	Asn
	Pro	Asp	Leu	Asp 820	Суѕ	Ser	Cys	Arg	Asp 825	Gly	Glu	Lys	Cys	Ala 830	His	His

	Ser	His	His 835		Thr	Leu	Asp	11e 840		Val	Gly	Cys	Thr 845	_	Leu	Asn
5	Glu	Asp		Gly	Val	Trp	Val 855		Phe	Lys	Ile	Lys 860	Thr	Gln	Asp	Gly
	His 865	Ala	Arg	Leu	Gly	Asn 870	Leu	Glu	Phe	Leu	Glu 875	Glu	Lys	Pro	Leu	Leu 880
10	Gly	Glu	Ala	Leu	Ala 885	Arg	Val	Lys	Arg	Ala 890	Glu	Lys	Lys	Trp	Arg 895	Asp
15	Lys	Arg	Glu	Lys 900	Leu	Gln	Leu	Glu	Thr 905	Asn	Ile	Val	Tyr	Lys 910	Glu	Ala
	Lys	Glu	Ser 915	Val	Asp	Ala	Leu	Phe 920	Val	Asn	Ser	Gln	Tyr 925	Asp	Arg	Leu
20	Gln	Val 930	Asp	Thr	Asn	Ile	Ala 935	Met	Ile	His	Ala	Ala 940	Asp	Lys	Arg	Val
	His 945	Arg	Ile	Arg	Glu	Ala 950	Tyr	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960
25 111 1-1	Val	Asn	Ala	Ala	Ile 965	Phe	Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala
√↓ UTI 3•0	Tyr	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn
	Asn	Gly	Leu 995	Leu	Cys	Trp	Asn	Val 1000	_	Gly	His	Val	Asp 1005		Glu	Glu
171 355 1-4	Gln	Asn 1010	Asn)	His	Arg	Ser	Val 1015		Val	Ile	Pro	Glu 1020	_	Glu	Ala	Glu
-	Val 1025		Gln	Glu		Arg 1030		Cys		_	Arg 1035	_	Tyr	Ile		Arg 1040
40	Val	Thr	Ala	Tyr	Lys 1045		Gly	Tyr	Gly	Glu 1050		Cys	Val	Thr	Ile 1055	
45	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 1065		Phe	Ser	Asn	Cys 1070		Glu
	Glu	Glu	Val 1075	_	Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 1085		Thr	Gly
50	Thr	Gln 1090	Glu)	Glu	Tyr	Glu	Gly 1095		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr
	Asp		Ala	Tyr	Gly	Asn		Pro	Ser	Val	Pro		Asp	Tyr	Ala	Ser

	Va	ıl Ty	yr Gl	lu Gl		/s Se .25	г Ту	r Th	ır As		y Ar 30	g Ar	g Gl	u As		o Cys	
5	Gl	u Se	er As		g Gl 40	у Ту	r Gl	y As	р Ту: 11		r Pr	o Le	u Pr	o Al 11		y Tyr	
	Va	l Th		s As 55	p Le	u Glı	ту:	r Ph		o Gli	u Thi	r Ası	2 Ly		l Tr	p Ile	
10	Gl	u Il 11	e Gl 70	y Gl	u Th	r Glu	117		r Phe	e Ile	e Val	Asp 118		r Val	l Gl	u Leu	
15	Le:		u Me	t Gli	u Gli	ı											-
	(2)	IN	FORM	MOITA	ı FOF	SEQ	ID	NO : 3	3:								
20		()	•	(A) L	ENGI	HARA	567	base	pai	rs							
			((C) S	TRAN	nuc DEDN OGY :	ESS:	sin									
		(ix	(AME/	KEY:		3567									
30		(xi) SE	QUEN	CE D	ESCR:	PTI	ON:	SEQ 1	D NO	0:3:						
	ATG Met 1	GAG Glu	GAA Glu	AAT Asn	AAT Asn 5	CAA Gln	AAT Asn	CAA Gln	TGC Cys	ATA Ile 10	CCT Pro	TAC Tyr	AAT Asn	TGT Cys	TTA Leu 15	AGT Ser	48
35	AAT Asn	CCT Pro	GAA Glu	GAA Glu 20	GTA Val	CTT Leu	TTG Leu	GAT Asp	GGA Gly 25	GAA Glu	CGG Arg	ATA Ile	TCA Ser	ACT Thr	GGT Gly	AAT Asn	96
40	TCA Ser	TCA Ser	ATT Ile 35	GAT Asp	ATT Ile	TCT Ser	CTG Leu	TCA Ser 40	CTT	GTT Val	CAG Gln	TTT Phe	CTG Leu 45	GTA	TCT Ser	AAC Asn	144
45						GGA Gly											192
50	GGA Gly 65	ATA Ile	GTT Val	GGC Gly	CCT Pro	TCT Ser 70	CAA Gln	TGG Trp	GAT Asp	GCA Ala	TTT Phe 75	CTA Leu	GTA Val	CAA Gln	ATT Ile	GAA Glu 80	240
-	CAA Gln	TTA Leu	ATT Ile	AAT Asn	GAA Glu 85	AGA Arg	ATA Ile	GCT Ala	GAA Glu	TTT Phe 90	GCT Ala	AGG Arg	AAT Asn	GCT Ala	GCT Ala 95	ATT Ile	288

	GCT	raa 1	TTA	GAA	GGA	ATT A	GGA	AAC	CAA:	TTC	TAA :	ATA	IAT A	GTG	GAA	GCA	336
	Ala	a Asn	1 Leu	Glu 100	_	' Leu	Gly	Asn	105		Asn	ılle	Yyr	110		ı Ala	
5	TTT	' AAA	GAA	TGG	GAA	GAA	GAT	CCT	AAT	AAT	CCA	GCA	ACC	AGG	ACC	AGA	384
	Phe	Lys	Glu 115		Glu	Glu	Asp	Pro 120		Asn	Pro	Ala	125	_	Thr	Arg	
	GTA	ATT	GAT	CGC	TTT	CGT	ATA	CTT	GAT	GGG	CTA	CTT	GAA	AGG	GAC	ATT	432
10			Asp	Arg									Glu				
	CCT	TCG	TTT	GAC	ATT	TCT	GGA	TTT	GAA	GTA	CCC	CTT	TTA	TCC	GTT	TAT	480
																Tyr -	
15	145					150					155					160	
	GCT	CAA	GCG	GCC	AAT	CTG	CAT	CTA	GCT	ATA	TTA	AGA	GAT	тст	GTA	ATT	528
				Ala													3.0
20					165					170					175		
	ттт	GGA	GAA	AGA	TGG	GGA	TTG	ACA	ACG	ΔΤΔ	דממ	GTC	דממ	GAA	אאר	тат	576
				Arg													3,0
ig.		_		180	_	_			185					190		•	
2 5 -	AAT	AGA	CTA	ATT	AGG	CAT	TTA	GAT	GAA	TAT	GCT	GAT	CAC	TGT	GCA	AAT	624
				Ile													
the offer			195					200					205				
LTI	ACG	TAT	AAT	CGG	GGA	TTA	AAT	AAT	TTA	CCG	AAA	TCT	ACG	TAT	CAA	GAT	672
3∯	Thr		Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Lys	Ser	Thr	Tyr	Gln	Asp	
ł		210					215					220					
7	TGG	ATA	ACA	TAT	AAT	CGA	TTA	CGG	AGA	GAC	TTA	ACA	TTG	ACT	GTA	TTA	720
IJ∏ 2 €=		Ile	Thr	Tyr	Asn	_	Leu	Arg	Arg	Asp		Thr	Leu	Thr	Val		
3 5] -	225					230					235					240	
				GCT													768
	Asp	Ile	Ala	Ala		Phe	Pro	Asn	Tyr		Asn	Arg	Arg	Tyr		Ile	
10					245					250					255		
. •	CAG	CCA	GTT	GGT	CAA	CTA	ACA	AGG	GAA	GTT	TAT	ACG	GAC	CCA	TTA	ATT	816
	Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile	
				260					265					270			
15	AAT	TTT	AAT	CCA	CAG	TTA	CAG	TCT	GTA	GCT	CAA	TTA	CCT	ACT	TTT	AAC	864
	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn	
			275					280					285				
	GTT	ATG	GAG	AGC	AGC	GCA	ATT	AGA	AAT	CCT	CAT	TTA	TTT	GAT	ATA	TTG	912
50	Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu	
		290					295					300					

		Asn					Thr					Val				TTT Phe 320	960
5						CGA Arg					Leu						1008
10						TAT Tyr											1056
15						GGA Gly											1104
						CAA Gln											1152
20																	
						GAA Glu 390											1200
25		_				GTT Val											1248
M	AAT	AGT	GTG	CCA	CCT	CGC	GAA	GGA	TAT	AGT	CAT	CGT	TTA	TGT	CAT	GCA	1296
30 C			Val			Arg											
35 14				_		TCT Ser	Gly										1344
						CGT Arg											1392
40						ATA Ile 470											1440
45	GGC Gly					ACA Thr											1488
50	CGA Arg		Asn			GGT Gly		Phe									1536

								_			 AGT Ser	1584
5		GAT Asp 530				Leu					GTG Val	1632
10		GGC Gly									ATA Ile 560	1680
15	_	GAG Glu									AAT Asn	1728
20=		TTT Phe										1776
**		CTA Leu										1824
25		ATT Ile 610										1872
30 mm		GAA Glu										1920
17 13 35/=		ATC Ile		Leu						Asp	_	1968
40		AAT Asn	Leu									2016
		GAA Glu										2064
45		AAT Asn 690										2112
50		CGT Arg										2160

				Asn			Pro			GAG Glu	2208
5			Tyr			_			Leu	AAA Lys	2256
10							ATC Ile				2304
15							AAA Lys			AAT Asn	2352
20							TCA Ser 795				2400
							CCA Pro				2448
25							GAA Glu				2496
30 2							GGA Gly				2544
5 3 5 14				Trp			ATT Ile				2592
40							GAA Glu 875				2640
							GAG Glu				2688
45							ATT Ile				2736
50	AAA Lys										2784

			. Asp					Met					Asp			GTT Val	2832
5		Arg	ATC				Tyr					Ser					2880
10			GCG Ala														2928
15			TTA Leu													AAT Asn -	2976
20			TTA Leu 995						Lys					Val			3024
			AAC Asn					Leu					Trp				3072
25 mm		Ser	CAA Gln				Val					Gly					3120
30 D			GCA Ala	Tyr		Glu					Gly					His	3168
353 4	_		GAA Glu		Asn			Glu							Val		3216
40			GTA Val 1075				Asn					Asn		Tyr			3264
	Thr		GAA Glu			Glu							Asn				3312
45		Glu	GCC Ala				Asn			Val		Ala			Ala		3360
50			GAA Glu	Glu		Ser			Asp		Arg					Cys	3408

					Gly					Thr					Gly	TAT Tyr	3456
5				Asp					Pro					Val		ATT	3504
10			Gly				GGA Gly 117	Thr					Ser			TTA Leu	3552
15		Leu	ATG Met													-	3567
20	(2)						ID 1										
20 () ()			(1) :	(A) (B)	LEI TYI	NGTH PE: a	RACTI : 118 amino GY: 1	39 am aci	nino ld		ls						
							E: pr) ID	NO : 4	l :					
30	Met 1	Glu	Glu	Asn	Asn 5	Gln	Asn	Gln	Cys	Ile 10	Pro	Tyr	Asn	Cys	Leu 15	Ser	
	Asn	Pro	Glu	Glu 20	Val	Leu	Leu	Asp	Gly 25	Glu	Arg	Ile	Ser	Thr 30	Gly	Asn	
3 5]	Ser	Ser	Ile 35	Asp	Ile	Ser	Leu	Ser 40	Leu	Val	Gln	Phe	Leu 45	Val	Ser	Asn	
40	Phe	Val 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp	
10	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe '75	Leu	Val	Gln	Ile	Glu 80	
45	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile	
	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala	
50	Phe	Lys	Glu 115	Trp	Glu	Glu	Asp	Pro 120	Asn	Asn	Pro	Ala	Thr 125	Arg	Thr	Arg	
	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile	

	145		Pne	Asp	11e	150	-	Pne	GIU	vai	155		Leu	Ser	vaı	160
5	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170		Arg	Asp	Ser	Val 175	Ile
10	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
10	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Cys	Ala	Asn
15	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Lys	Ser 220	Thr	Tyr	Gln	Asp
	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
20	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile
25 <u>.</u>	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265	Val	Tyr	Thr	Asp	Pro 270	Leu	Ile
# ## ### #############################	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
30 T	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
r r	Asn 305	Asn	Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315	Val	Gly	Arg	Asn	Phe 320
3 5 Л СЭ	Tyr	Trp	Gly	Gly	His 325	Arg	Val	Ile	Ser	Ser 330	Leu	Ile	Gly	Gly	Gly 335	Asn
40	Ile	Thr	Ser	Pro 340	Ile	Tyr	Gly	Arg	Glu 345	Ala	Asn	Gln	Glu	Pro 350	Pro	Arg
	Ser	Phe	Thr 355	Phe	Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365	Asn	Pro	Thr
45	Leu	Arg 370	Leu	Leu	Gln	Gln	Pro 375	Trp	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
	Gly 385	Val	Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
50	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys. 430	His	Ala

	Thi	Phe	435		Arg	Ser	Gly	Thr 440		Phe	. Leu	Thr	Thr 445	•	/ Val	Val
5	Ph∈	Ser 450		Thr	His	Arg	Ser 455		Thr	Leu	Thr	Asn 460		Ile	Asp	Pro
10	Glu 465		Ile	Asn	Gln	Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe 490	Thr	Gly	Gly	Asp	Ile 495	Leu
15	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn -
	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe	Arg	Tyr 525	Ala	Ser	Ser
20 () ()	Arg	Asp 530	Ala	Arg	Val	Ile	Val 535	Leu	Thr	Gly	Ala	Ala 540	Ser	Thr	Gly	Val
1 2 5 U	Gly 545	Gly	Gln	Val	Ser	Val 550	Asn	Met	Pro	Leu	Gln 555	Lys	Thr	Met	Glu	Ile 560
There is all the state of the s	Gly	Glu	Asn	Leu	Thr 565	Ser	Arg	Thr	Phe	Arg 570	Tyr	Thr	Asp	Phe	Ser 575	Asn
30 <u> </u>	Pro	Phe	Ser	Phe 580	Arg	Ala	Asn	Pro	Asp 585	Ile	Ile	Gly	Ile	Ser 590	Glu	Gln
	Pro	Leu	Phe 595	Gly	Ala	Gly		Ile 600	Ser	Ser	Gly	Glu	Leu 605	Tyr	Ile	Asp
3 <i>5</i> €⊒ }=	Lys	Ile 610	Glu	Ile	Ile		Ala 615	Asp	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp
‡ 0	Leu 625	Glu	Arg	Ala	Gln	Lys 630	Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
	Gln	Ile	Gly		Lys 645	Thr	Asp	Val		Asp 650	Tyr	His	Ile	Asp	Gln 655	Val
15	Ser	Asn		Val 660	Asp	Cys	Leu		Asp 665	Glu	Phe	Cys	Leu	Asp 670	Glu	Lys
	Arg	Glu	Leu 675	Ser	Glu	Lys		Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
50	Arg	Asn 690	Leu	Leu	Gln		Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
	Asp 705	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp

	Asp	Val	Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730		Gly	Thr	Val	Asp 735		
5	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745		Asp	Glu	Ser	Lys 750	Leu	Lys	
10	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	Arg 760	Gly	Tyr	Ile	Glu	Asp 765	Ser	Gln	Asp	
10	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn	•
15	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800	
	Gly	Lys	Cys	Gly	Glu 805	Pro	Asn	Arg	Cys	Ala 810	Pro	His	Leu	Glu	Trp 815	Asn	
20 (3 (3 (4)	Pro	Asp	Leu	Asp 820	Сув	Ser	Cys	Arg	Asp 825	Gly	Glu	Lys	Cys	Ala 830	His	His	
.0 ~] 25	Ser	His	His 835	Phe	Thr	Leu	Asp	Ile 840	Asp	Val	Gly	Cys	Thr 845	Asp	Leu	Asn	
	Glu	Asp 850	Leu	Gly	Val	Trp	Val 855	Ile	Phe	Lys	Ile	Lys 860	Thr	Gln	Asp	Gly	
30 []	His 865	Ala	Arg	Leu	Gly	Asn 870	Leu	Glu	Phe	Leu	Glu 875	Glu	Lys	Pro		Leu 880	
D N	Gly	Glu	Ala	Leu	Ala 885	Arg	Val	Lys	Arg	Ala 890	Glu	Lys	Lys	Trp	Arg 895	Asp	
35	Lys	Arg	Glu	Lys 900	Leu	Gln	Leu	Glu	Thr 905	Asn	Ile	Val	Tyr	Lys 910	Glu	Ala	
40	Lys	Glu	Ser 915	Val	Asp	Ala	Leu	Phe 920	Val	Asn	Ser	Gln	Tyr 925	Asp	Arg	Leu	
	Gln	Val 930	Asp	Thr	Asn	Ile	Ala 935	Met	Ile	His	Ala	Ala 940	Asp	Lys	Arg	Val	
45	His 945	Arg	Ile	Arg	Glu	Ala 950	Tyr	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960	
	Val	Asn	Ala	Ala	Ile 965	Phe	Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala	
50	Tyr	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn	
	Asn	Gly	Leu 995	Leu	Cys	Trp	Asn	Val		Gly	His	Val	Asp 1005		Glu	Glu	

-2567

	Gln	Asn 101		His	Arg	Ser	Val 101		Val	Ile	Pro	Glu 102	-	Glu	Ala	Glu
5	Val 102		Gln	Glu	Val	Arg 103		Cys	Pro	Gly	Arg		Tyr	Ile	Leu	Arg
10	Val	Thr	Ala	Tyr	Lys 104		Gly	Tyr	Gly	Glu 105	_	Cys	Val	Thr	Ile 105	
10	Glu	Ile	Glu	Asp		Thr	Asp	Glu	Leu 106	_	Phe	Ser	Asn	Cys 1070		Glu
15	Glu	Ģlu	Val 107		Pro	Asn	Asn	Thr		Thr	Cys	Asn	Asn 1085	_	Thr	Gly
	Thr	Gln 109	Glu O	Glu	Tyr	Glu	Gly 1095		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr
20 11 11	Asp 1109		Ala	Tyr	Gly	Asn 1110		Pro	Ser	Val	Pro 1115		Asp	Tyr	Ala	Ser 1120
.⊡ `↓ [2 5	Val	Tyr	Glu	Glu	Lys 1125		Tyr	Thr	Asp	Gly 1130	_	Arg	Glu	Asn	Pro 1135	-
	Glu	Ser	Asn	Arg 1140	_	Tyr	Gly	Asp	Tyr 1145		Pro	Leu	Pro	Ala 1150	_	Tyr
• •30 •2	Val	Thr	Lys 1155	-	Leu	Glu	Tyr	Phe 1160		Glu	Thr	Asp	Lys 1165		Trp	Ile
[]	Glu	Ile 1170	Gly	Glu	Thr		Gly 1175		Phe	Ile		Asp 1180		Val	Glu	Leu
1 3 5	Leu 1185		Met	Glu	Glu											
40	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10 : 5 :								
		(i)	(B) LE	NGTH	: 35 nucl	67 b eic	ase acid	pair I	s						
45					RAND POLO			_	rle							
		(ix)) NA	: ME/K CATI			567								
50		(xi)	SEQ						EQ I	D NC):5:					

		Glu		Gln			Pro			AGT Ser		48
5							CGG Arg		Gly	AAT Asn		96
10							CAG Gln				1	L44
15		_	_				TTA Leu				1	L92
20	_		_				TTT Phe 75				2	40
20 点 点							GCT Ala				2	88
25 1-							AAT Asn				3	36
30							CCA Pro				3	84
	GTA Val									ATT Ile		32
40	CCT Pro 145						CCC Pro 155				4	80
	GCT Ala		-				TTA Leu				5	28
45							AAT Asn				5	76
50	AAT Asn						GCT Ala				6	24

		' AAT ' Asn						Thr		672
5		ACA Thr								720
10		GCC Ala								768
15		GTT Val								816
20		AAT Asn 275								864
29 13 13 14		GAG Glu								912
		CTT Leu								960
		GGA Gly	Gly						_	1008
35		TCT								1056
40		ACT Thr 355								1104
		TTA Leu	+							1152
45		G AA Glu								1200
50		AGA Arg								1248

					Pro					Sez					s His	r GCA s Ala	1296
5				Gln					Pro					Gly		GTA Val	1344
10			Trp										Thr			CCA Pro	1392
. 15		Arg	ATT Ile														1440
20			TCT Ser														1488
20 50 5 1			AAT Asn														1536
25			ATT Ile 515														1584
30 mm mm m	Arg	Asp 530	GCA Ala	Arg	Val	Ile	Val 535	Leu	Thr	Gly	Ala	Ala 540	Ser	Thr	Gly	Val	1632
17 25			CAA Gln		Ser												1680
40			AAC ' Asn '	Leu '			–		Phe							AAT Asn	1728
			TCA Ser					Pro									1776
45			TTT (Phe (595				Ser					Glu					1824
50	Lys		GAA /			Leu .					Phe						1872

	TTA Leu 625	ı Glı	A AGA	A GCZ g Ala	A CAA	A AAC 1 Lys 630	a Ala	GT(G AA'	r GCG n Alá	C CTC a Let 635	ı Phe	T AC	r TC	r TCC	C AAT C Asn 640	1920
5	CAA Gln	ATC Ile	GGC Gly	TTA Leu	A AAA 1 Lys 645	Thr	GAT Asp	GTC Val	ACC Thr	GAT Asp 650	Tyr	CAT His	T ATT	GAT Asp	CAA Glr 655	GTA Val	1968
10	TCC Ser	AAT	TTA Leu	GTG Val 660	Asp	TGT Cys	TTA Leu	TCA Ser	GAT Asp 665	Glu	TTT Phe	TGT Cys	CTG Leu	GAT Asp 670	Glu	AAG Lys	2016
15	CGA Arg	GAA Glu	TTG Leu 675	TCC Ser	GAG Glu	AAA Lys	GTC Val	AAA Lys 680	CAT His	GCG Ala	AAG Lys	CGA Arg	CTC Leu 685	AGT Ser	GAT Asp	GAG Glu	2064
20	CGG Arg	AAT Asn 690	TTA Leu	CTT Leu	CAA Gln	GAT Asp	CCA Pro 695	AAC Asn	TTC Phe	AGA Arg	GGG Gly	ATC Ile 700	AAT Asn	AGA Arg	CAA Gln	CCA Pro	2112
20 10 10 13 25	GAC Asp 705	CGT Arg	GGC Gly	TGG Trp	AGA Arg	GGA Gly 710	AGT Ser	ACA Thr	GAT Asp	ATT Ile	ACC Thr 715	ATC Ile	CAA Gln	GGA Gly	GGA Gly	GAT Asp 720	2160
25	GAC Asp	GTA Val	TTC Phe	AAA Lys	GAG Glu 725	AAT Asn	TAC Tyr	GTC Val	ACA Thr	CTA Leu 730	CCG Pro	GGT Gly	ACC Thr	GTT Val	GAT Asp 735	GAG Glu	2208
30 10	TGC Cys	TAT Tyr	CCA Pro	ACG Thr 740	TAT Tyr	TTA Leu	TAT Tyr	CAG Gln	AAA Lys 745	ATA Ile	GAT Asp	GAG Glu	TCG Ser	AAA Lys 750	TTA Leu	AAA Lys	2256
	GCT Ala	Tyr	ACC Thr 755	CGT Arg	TAT Tyr	GAA Glu	Leu .	AGA Arg 760	GGG Gly	TAT Tyr	ATC Ile	G AA Glu	GAT Asp 765	AGT Ser	CAA Gln	GAC Asp	2304
40	TTA (GAA Glu 770	ATC Ile	TAT Tyr	TTG . Leu	Ile .	CGT ' Arg '	TAC .	AAT Asn	GCA Ala	Lys	CAC His 780	GAA Glu	ATA Ile	GTA Val	AAT Asn	2352
	GTG (Val) 785	CCA Pro	GGC Gly	ACG ·	Gly	TCC ' Ser : 790	TTA ' Leu '	rgg Frp	CCG Pro	Leu	TCA Ser 795	GCC Ala	CAA Gln	AGT Ser	Pro	ATC Ile 800	2400
45	GGA A	AAG Lys	TGT (Gly	GAA Glu: 805	CCG /	AAT (Asn)	CGA '	Cys	GCG Ala 810	CCA Pro	CAC His	CTT Leu	Glu	TGG Trp 815	AAT Asn	2448
50	CCT (GAT (Leu .	GAT (Asp (TGT '	TCC '	TGC i	Arg .	GAC Asp 825	GGG Gly	GAA . Glu	AAA Lys	Cys	GCA Ala 830	CAT His	CAT His	2496

													AAT Asn	2544
5		Leu											 GGC	2592
10									GAA Glu 875				_	2640
15									GAG Glu					2688
20		_			_				ATT Ile					2736
						Leu			TCT Ser					2784
25									GCG Ala					2832
<u> </u>				Glu					TTG Leu 955					2880
			Ala						GGA Gly					2928
40		Leu							AAA Lys					2976
			_			Asn		Lys	CAT His			Val		3024
45		Asn			Ser		Leu		CCA Pro		Trp			3072
50	Ser					Val			CGT Arg 1035	Gly				3120

																CAT	3168
	Val	Thr	Ala	Tyr	Lys 104		Gly	Tyr	· Gly	/ Glu 105	_	Cys	Val	Thr	105	His	
5					Asn					Lys					Val	GAA Glu	3216
10				Tyr					Val					Tyr		GGG Gly	3264
15			GAA Glu 0					Thr					Asn				3312
20		Glu	GCC Ala				Asn					Ala					3360
20 0 0 10 V			GAA Glu			Ser					Arg					Cys	3408
25 - - []			AAC Asn		Gly					Thr					Gly		3456
3.0			AAG Lys 1155	Asp					Pro					Val			3504
			GGA Gly					Thr					Ser				3552
40		Leu	ATG Met														3567
	(2)	INFO	RMAT	ION	FOR	SEQ	ID N	O:6:									
45		((i) S	(A) (B)	LEN TYP	CHAR GTH: E: a OLOG	118 mino	9 am aci	ino d		ls						
50			i) M				_) ID	NO : 6	i :					
	Met 1		Glu										Asn	Cys	Leu 15	Ser	

	Asn	Pro	GIU	20	vaı	Leu	Leu	Asp	25 25	GIU	Arg	116	ser	30	GIY	ASI
5	Ser	Ser	Ile 35	Asp	Ile	Ser	Leu	Ser 40	Leu	Val	Gln	Phe	Leu 45	Val	Ser	Asr
10	Phe	Val 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp
10	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe 75	Leu	Val	Gln	Ile	Glu 80
15	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile
	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala
20 다	Phe	Lys	Glu 115	Trp	Glu	Glu	Asp	Pro 120	Asn	Asn	Pro	Ala	Thr 125	Arg	Thr	Arg
10 25	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile
* * * * * * * * * * * * * * * * * * * 	Pro 145	Ser	Phe	Arg	Ile	Ser 150	Gly	Phe	Glu	Val	Pro 155	Leu	Leu	Ser	Val	Tyr 160
₩ \$ <u>0</u>	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170	Leu	Arg	Asp	Ser	Val 175	Ile
	Phe	Gly	Glu	Ala 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
15	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Cys	Ala	Asn
40	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Lys	Ser 220	Thr	Tyr	Gln	Asp
70	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
45	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile
	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265	Val	Tyr	Thr	Asp	Pro 270	Leu	Ile
50	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu

	Asn 305		Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315		Gly	Arg	Asn	Phe 320
5	Tyr	Trp	Gly	Gly	His 325	Arg	Val	Ile	Ser	Ser 330	Leu	Ile	Gly	Gly	Gly 335	Asn
10	Ile	Thr	Ser	Pro 340	Ile	Tyr	Gly	Arg	Glu 345	Ala	Asn	Gln	Glu	Pro 350	Pro	Arg
••	Ser	Phe	Thr 355	Phe	Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365	Asn	Pro	Thr
15	Leu	Arg 370	Leu	Leu	Gln	Gln	Pro 375	Trp	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
	Gly 385	Val	Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
220 	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
\ [U 25	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys 430	His	Ala
	Thr	Phe	Val 435	Gln	Arg	Ser	Gly	Thr 440	Pro	Phe	Leu	Thr	Thr 445	Gly	Val	Val
30		Ser 450	Trp	Thr	His	Arg	Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro
	Glu 465	Arg	Ile	Asn	Gln	Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
35	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe 490	Thr	Gly	Gly	Asp	Ile 495	Leu
40	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn
	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe	Arg	Tyr 525	Ala	Ser	Ser
45	Arg	Asp 530	Ala	Arg	Val	Ile	Val 535	Leu	Thr	Gly	Ala	Ala 540	Ser	Thr	Gly	Val
	Gly 545	Gly	Gln	Val	Ser	Val 550	Asn	Met	Pro	Leu	Gln 555	Lys	Thr	Met	Glu	Ile 560
50	Gly	Glu	Asn	Leu	Thr 565	Ser	Arg	Thr	Phe	Arg 570	Tyr	Thr	Asp	Phe	Ser 575	Asn
	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly	Ile	Ser	Glu	Gln

	Pro	Leu	Phe 595	_	Ala	Gly	Ser	Ile 600		Ser	Gly	Glu	Leu 605	_	Ile	Asp
5	Lys	Ile 610		Ile	Ile	Leu	Ala 615	-	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp
10	Leu 625	Glu	Arg	Ala	Gln	Lys 630	Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
	Gln	Ile	Gly	Leu	Lys 645	Thr	Asp	Val	Thr	Asp 650	Tyr	His	Ile	Asp	Gln 655	Val
15	Ser	Asn	Leu	Val 660	Asp	Cys	Leu	Ser	Asp 665	Glu	Phe	Суз	Leu	Asp 670	Glu	Lys
	Arg	Glu	Leu 675	Ser	Glu	Lys	Val	Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
20 \0 \0	Arg	Asn 690	Leu	Leu	Gĺn	Asp	Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
10 25	Asp 705	Arg	Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	Asp 720
really green	Asp	Val	Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp 735	Glu
30	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745	Ile	Asp	Glu	Ser	Lys 750	Leu	Lys
The state of the s	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	Arg 760	Gly	Tyr	Ile		Asp 765	Ser	Gln	Asp
35	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn
40	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800
	Gly	Lys	Сув	Gly	Glu 805	Pro	Asn	Arg	Cys	Ala 810	Pro	His	Leu	Glu	Trp 815	Asn
45	Pro	Asp	Leu	Asp 820	Cys	Ser	Cys	Arg	Asp 825	Glγ	Glu	Lys	СЛа	Ala 830	His	His
	Ser	His	His 835	Phe	Thr	Leu	Asp	Ile 840	Asp	Val	Gly	Сув	Thr 845	Asp	Leu	Asn
50	Glu	Asp 850	Leu	Gly	Val	Trp	Val 855	Ile	Phe	Lys	Ile	Lys 860	Thr	Gln	Asp	Gly
	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	ГЛа	Pro	Leu	Leu

	Gly	/ Glu	ı Ala	Leu	885		Val	. Lys	Arg	890		Lys	Lys	Trp	Arg 895	Asp
5	Lys	Arg	Glu	Lys 900		Gln	Leu	Glu	Thr 905		Ile	Val	Tyr	Lys 910		Ala
10	Lys	Glu	Ser 915		Asp	Ala	Leu	Phe 920	Val	Asn	Ser	Gln	Tyr 925	_	Arg	Leu
,	Gln	Val 930		Thr	Asn	Ile	Ala 935	Met	Ile	His	Ala	Ala 940	Asp	Lys	Arg	Val
15	His 945		Ile	Arg	Glu	Ala 950	Tyr	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960
	Val	Asn	Ala	Ala	Ile 965	Phe	Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala
20 ()	туг	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn
10 25	Asn	Gly	Leu 995	Leu	Cys	Trp	Asn	Val 1000	-	Gly	His	Val	Asp 1005		Glu	Glu
* <u></u>	Gln	Asn 1010		His	Arg	Ser	Val 1015		Val	Ile	Pro	Glu 1020	_	Glu	Ala	Glu
10 30	Val 1025		Gln	Glu	Val	Arg 1030		Cys	Pro	Gly	Arg 1035		Tyr	Ile	Leu	Arg 1040
Man dent des	Val	Thr	Ala	Tyr	Lys 1045		Gly	Tyr	Gly	Glu 1050	Gly	Cys	Val		Ile 1055	
\$ 5 ±	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 1065		Phe	Ser	Asn	Cys 1070		Glu
40	Glu	Glu	Val 1075		Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 1085	-	Thr	Gly
	Thr	Gln 1090		Ģlu	Tyr	Glu	Gly 1095		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr
45	Asp 1105		Ala	Tyr	Gly	Asn 1110		Pro	Ser	Val	Pro 1115		Asp	Tyr	Ala	Ser 1120
	Val	Tyr	Glu		Lys 1125		Tyr	Thr	Asp	Gly 1130	Arg	Arg	Glu	Asn	Pro 1135	-
50	Glu	Ser	Asn	Arg 1140		Tyr	Gly	Asp	Tyr 1145		Pro	Leu	Pro	Ala 1150		Tyr
	Val	Thr	Lys 1155	_	Leu	Glu	Tyr	Phe 1160		Glu	Thr	Asp	Lys 1165		Trp	Ile

5	Leu 118	Leu 5	Met	Glu	ı Glu	1											
10	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO :7	':								
		(i) SE	QUEN	CE C	HARA	CTER	ISTI	CS:								
						H: 3			_	rs							
			-			nuc DEDN				•							
15						OGY:			520								
		(ix		ATUR		V131.	CDC										
						KEY:		3567									
20				_, _													
		(xi)) SE(QUEN	CE D	ESCR:	IPTI	ON:	SEQ	ID N	0:7:						
Ō	ATG	GAG	GAA	AAT	AAT	CAA	AAT	CAA	TGC	ATA	CCT	TAC	AAT	TGT	TTA	AGT	48
4		Glu	Glu	Asn		Gln	Asn	Gln	Cys		Pro	Tyr	Asn	Cys		Ser	
4)	1				5					10					15		
.d	AAT	CCT	GAA	GAA	GTA	CTT	TTG	GAT	GGA	GAA	CGG	ATA	TCA	ACT	GGT	AAT	96
n						Leu											
				20					25					30			
30	TCA	TCA	ATT	GAT	ATT	TCT	CTG	TCA	СТТ	GTT	CAG	ттт	CTG	ата	тст	AAC	144
]						Ser											
ed M			35					40					45				
Ī	an entren	CITA	CCA	~~~	CCA	CC3	- THE PERSON NAMED IN	תיתי א	C TTTT	CCA	mm y	202	CAT	- Transm	CTD	TCC	100
rain						GGA Gly											192
		50	7	1	- -1	1	55			1		60					
	CCA	אידא	Cuture	ccc	CCT	TCT	C	Trans	CAT	CCA	ششش	CTA	CTA	C	አ ጥጥ	CAA	240
10						Ser											240
	65			1		70					75					80	
	<i>a.</i>	mm s	1 mm		~~~			0.0m	<i>a</i>	aaa	0.0m			a a m	aam	» mm	200
						AGA Arg											288
15	GIL	2Cu	***	-wii	85	9	110	ALG	914	90	1114	AL 9	7,011		95	110	
						TTA											336
	Ala	ASII	Leu	100	GIA	Leu	GIA	ASII	105	Pne	ASII	TTE	TYE	110	GIU	Ala	
50																	
						GAT											384
	Phe	Lys	Glu	-	Glu	Asp	Asp	Pro		Asn	Pro	Thr	Thr	Arg	Thr	Arg	
			, , ¬					, , , , ,					1 /. "				

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu

1180

1175

1170

			Asp				Leu			i Glu		ATT Ile	4	32
5		Ser							Leu			TAT Tyr 160	4	80
10	_	_	GCG Ala										5:	28
15			GAA Glu										5	76
20			CTA Leu 195	_		_							62	24
			AAT Asn										67	12
25! 		_	ACA Thr										72	20
3 0			GCC Ala										76	8
35.			GTT Val				Arg						81	6
40			AAT Asn 275			Gln							86	4
40			GAG Glu	-	Ala								91	.2
45			CTT Leu									Phe	96	0
50			GGA Gly					 					100	8

				Ile			Ala	AAC Asn			Pro	AGA Arg	1056
5								ACT Thr		Asn			1104
10								CCA Pro					1152
. 15								ACA Thr 395					1200
20								GAA Glu					1248
								CAT His					1296
25 mg mg								TTA Leu					1344
**************************************	_							ACA Thr					1392
35								GGA Gly 475					1440
40								ACA Thr					1488
			-					CTA Leu					1536
45								TTT Phe					1584
50								GCG Ala					1632

	Gly			GTA Val 550				Lys		ATA Ile 560	1680
5				TCT Ser							1728
10				GCT Ala							1776
15				GGT Gly							1824
<i>=</i> 3 ∙0		_		CTA Leu							1872
20 10 10 12 25				AAG Lys 630							1920
r Jan				ACC Thr							1968
				TGT Cys							2016
111 121 35				AAA Lys	Val						2064
40				GAT Asp							2112
			-	GGA Gly 710							2160
45				AAT Asn							2208
50				TTA Leu							2256

				Arg				Gly				Ser	A GAC Asp	2304
5			Ile								Glu		AAT Asn	2352
10		Pro			TCC Ser 790								ATC Ile 800	2400
15					CCG Pro									2448
20					TCC Ser									2496
ā					TTG Leu									2544
					TGG Trp									2592
30 C C C					AAT Asn 870									2640
15 35				Leu	CGT Arg									2688
40					CAG Gln		Glu							2736
	AAA Lys			-		Leu				Gln				2784
45					ATC Ile									2832
50					GCG Ala 950									2880

			GCG Ala			Phe											2928
5			TTA Leu							Ile					Phe		2976
10			TTA Leu 995						Lys					Val			3024
15			AAC Asn					Leu					Trp				3072
20		Ser	CAA Gln				Val					Gly					3120
20 5 5			GCA Ala			Glu					Gly					His	3168
			GAA Glu		Asn					Lys					Val		3216
17 130 13			GTA Val 1075	Tyr			Asn		Val					Tyr			3264
	Thr		GAA Glu			Glu		Thr			Ser		Asn				3312
40		Glu	GCC Ala		Gly					Val		Ala					3360
40			GAA Glu	-		Ser										CAa	3408
45			AAC Asn		Gly					Thr					Gly		3456
50			AAG Lys 1155	qeA					Pro					Val			3504

			e Gly					/ Thi					Ser			A TTA Leu	3552
5		Let		G GAG													3567
10	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 8	:								
15			(i)	(B) LE) TY	CHA NGTH PE: POLO	: 11 amin	89 a o ac	mino iđ		ds						
				MOLE: SEQUI			_			מז כ	NO · i	ą <i>,</i>					
3 0 D	Met 1			Asn						-			Asn	Cys	Leu 15	Ser	
0 1 1 2 2 5	Asn	Pro	Glu	Glu 20	Val	Leu	Leu	Asp	Gly 25	Glu	Arg	Ile	Ser	Thr 30	Gly	Asn	
	Ser	Ser	Ile 35	Asp	Ile	Ser	Leu	Ser 40	Leu	Val	Gln	Phe	Leu 45	Val	Ser	Asn	
10 3	Phe	Val 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp	
]]] } 5	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe 75	Leu	Val	Gln	Ile	Glu 80 -	
,,,	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile	
4 0	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala	
	Phe	Lys	Glu 115	Trp	Glu	Asp	Asp	Pro 120	His	Asn	Pro	Thr	Thr 125	Arg	Thr	Arg	
1 5	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile	
50	Pro 145	Ser	Phe	Arg	Ile	Ser 150	Gly	Phe	Glu	Val	Pro 155	Leu	Leu	Ser	Val	Tyr 160	
. -	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170	Leu	Arg	Asp	Ser	Val 175	Ile	

	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185		Asn	Val	Asn	Glu 190	Asn	Tyr
5	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Cys	Ala	Asn
	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Lys	Ser 220	Thr	Tyr	Gln	Asp
10	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
15	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile
	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265	Val	Tyr	Thr	Asp	Pro 270	Leu	Ile
20 []	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
25 - -	Asn 305	Asn	Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315	Val	Gly	Arg	Asn	Phe 320
iñ 10	Tyr	Trp	Gly	Gly	His 325	Arg	Val	Ile	Ser	Ser 330	Leu	Ile	Gly	Gly	Gly 335	Asn
	Ile	Thr	Ser	Pro 340	Ile	Tyr	Gly	Arg	Glu 345	Ala	Asn	Gln	Glu	Pro 350	Pro	Arg
15 15	Ser	Phe	Thr 355	Phe	Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365	Asn	Pro	Thr
	Leu	Arg 370	Leu	Leu	Gln	Gln	Pro 375	Trp	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
40	Gly 385	Val	Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
45	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Суз 430	His	Ala
50	Thr	Phe	Val 435	Gln	Arg	Ser	Gly	Thr 440	Pro	Phe	Leu	Thr	Thr 445	Gly	Val	Val
	Phe	Ser 450	Trp	Thr	His	Arg	Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro

	465		ille	: ASI	GIN	470		Leu	vaı	. гуз	475		Arg	r vai	. Trp	480
5	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe		Gly	Gly	Asp	1le 495	
	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn
10	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe	Arg	Tyr 525	Ala	Ser	Ser
15	Arg	Asp 530	Ala	Arg	Val	Ile	Val 535	Leu	Thr	Gly	Ala	Ala 540	Ser	Thr	Gly	Val
	Gly 545	Gly	Gln	Val	Ser	Val 550	Asn	Met	Pro	Leu	Gln 555	Lys	Thr	Met	Glu	Ile 560
20 	Gly	Glu	Asn	Leu	Thr 565	Ser	Arg	Thr	Phe	Arg 570	Tyr	Thr	Asp	Phe	Ser 575	Asn
0	Pro	Phe	Ser	Phe 580	Arg	Ala	Asn	Pro	Asp 585	Ile	Ile	Gly	Ile	Ser 590	Glu	Gln
25 -	Pro	Leu	Phe 595	Gly	Ala	Gly	Ser	Ile 600	Ser	Ser	Gly	Glu	Leu 605	Tyr	Ile	Asp
₩ 30	Lys	Ile 610	Glu	Ile	Ile	Leu	Ala 615	Asp	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp
	Leu 625	Glu	Arg	Ala	Gln	Lys 630	Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
[] 35	Gln	Ile	Gly	Leu	Lys 645	Thr	Asp	Val	Thr	Asp 650	Tyr	His	Ile	Asp	Gln 655	Val
	Ser	Asn		Val 660	Asp	Суз	Leu	Ser	Asp 665	Glu	Phe	Cys	Leu	Asp 670	Glu	Lys
40	Arg	Glu	Leu 675	Ser	Glu	Lys	Val	Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
45	Arg	Asn 690	Leu	Leu	Gln	_	Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
	Asp 705	Arg	Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	Asp 720
50	Asp	Val	Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp 735	Glu
	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys

5	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 106		Phe	Ser	Asn	Cys 1070		Glu	
	Glu	Glu	Val 1075	-	Pro	Asn	Asn	Thr 108	Val	Thr	Cys	Asn	Asn 1085		Thr	Gly	
10	Thr	Gln 1090		Glu	Tyr	Glu	Gly 1099		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr	
1.5	Asp		Ala	Tyr	Gly	Asn 1110		Pro	Ser	Val	Pro		Asp	Tyr	Ala	Ser 1120	
15	Val	Tyr	Glu	Glu	Lys 1125		Tyr	Thr	Asp	Gly 1130		Arg	Glu	Asn	Pro 1135		
20	Glu	Ser	Asn	Arg 1140		Tyr	Gly	Asp	Tyr 1145		Pro	Leu	Pro	Ala 1150		Tyr	
20 11 13	Val	Thr	Lys 1155		Leu	Glu	Tyr	Phe 1160	Pro	Glu	Thr	Asp	Lys 1165		Trp	Ile	
2 5 	Glu	Ile 1170	_	Glu	Thr	Glu	Gly 1175		Phe	Ile	Val	Asp 1180		Val	Glu	Leu	
\. !T 30	Leu 1185	Leu	Met	Glu	Glu												
	(2)		SEC (A (E	QUENC A) LE B) TY	FOR CE CH CNGTH CPE: CRANE	IARACI: 35 nucl	CTERI 567 b Leic ESS:	STIC ase acid	CS: pair l	s							
40		(ix)		A) NA	E: AME/F DCATI			3567									
45		(xi)) SE(QUENC	CE DI	ESCR:	IPTIC	ON: 5	SEQ I	ID NO	0:9:						
									TGC Cys								4.6
50									GGA Gly 25						Gly		96

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Il His

1050

			_												AAC Asn	144
5	արդուր	CTA	35		CCA	CCN	ጥጥጥ	4.0		CCA	ጥጥለ	מידי מ	45 Cam	רייים	TGG	192
J			Pro					Leu					Asp			192
10			GTT Val													240
15			ATT Ile							_						288
<u> </u>			TTA Leu													336
			GAA Glu 115													384
25		-	GAT Asp													432
			TTT Phe													480
13 14 35			GCG Ala													528
40			GAA Glu	Arg	Trp		Leu	Thr	Thr	Ile			Asn			576
70			CTA Leu 195													624
45			AAT Asn													672
50			ACA Thr													720

						Phe					Asr				A ATT o Ile		768
5					Gln									Leu	ATT Ile		816
10			AAT Asn 275												AAC Asn		864
15			GAG Glu														912
20			CTT Leu														960
			GGA Gly														1008
25			TCT Ser					Arg									1056
30			ACT Thr 355				Pro '										1104
13 35			TTA Leu			Gln					Pro						1152
40			GAA (Val					Pro				 	TAT Tyr 400		1200
			AGA (Gly					Leu								1248
45	AAT Asn		Val					Gly '					Leu				1296
50	ACT Thr	Phe	GTT (Val (435				Gly :					Thr				~	1344

		Trp							Thr		CCA Pro	1392
5									AGA Arg			1440
10	 			 		-	-		GGG Gly			1488
. 15									GTC Val			1536
20									TAC Tyr 525			1584
Here Man Hard House									TCC Ser			1632
2 5 4									ACT Thr			1680
30									GAT Asp			1728
35									ATA Ile			1776
40					Ser				CTT Leu 605			1824
40			-						GCA Ala			1872
45									ACT Thr			1920
50									ATT Ile			1968

				Asp			Glu			Glu	AAG Lys	2016
5		TTG Leu 675										2064
10		TTA Leu										2112
15		GGC										2160
20		TTC Phe										2208
20 5 5 4		CCA Pro										2256
25 14 14 17		ACC Thr 755			Leu							2304
30		ATC Ile										2352
175		GGC Gly								Pro		2400
40		TGT Cys	Gly				Ala		Glu			2448
		CTA Leu	-			Arg						2496
45		CAT His 835			Asp							2544
50		TTA Leu										2592

	Ala					Leu					Glu				TTA Leu 880	2640
5			CTA Leu													2688
10			AAA Lys 900													2736
15			GTA Val													2784
20			ACG Thr													2832
20 0 0 7			CGG Arg		_											2880
25 -4 -4 -4 -4 -4 -4 -4 -4 -4 -4 -4 -4 -4			GCC Ala									-	–			2928
30 C			TAT Tyr 980		_											2976
			TTA Leu					Lys					Val		GAG Glu ~	3024
40		Asn	CAC His				Leu					Trp				3072
	Ser		GAG Glu			Val					Gly					3120
45	 		TAT Tyr		Glu				_	Gly					His	3168
50	 		GAC Asp 1060	Asn					Lys					Val		3216

				Tyr					Val					Tyr		GGG Gly	3264
5			Glu	GAA Glu				Thr					Asn				3312
10		Glu		TAT Tyr			Asn					Ala					3360
15				GAA Glu		Ser					Arg					Cys	3408
20				AGA Arg 1140	Gly					Thr					Gly		3456
				GAT Asp					Pro			Asp		Val			3504
25			Gly	GAA Glu				Thr			Val		Ser				3552
30 171 1		Leu		GAG Glu	_												3567
Hard Street Land Ball	(2)			ION													
40		·		(A) (B)	LEN TYP	GTH: E: a	118 mino Y: 1	9 am aci	ino d		s						
. •				OLEC			-										
45				EQUE									_	~	_		
43	Met 1	GIu	Glu	Asn	Asn 5	Gin	Asn	Gin	Cys	10	Pro	Tyr	Asn	Cys	Leu 15	Ser	
50	Asn	Pro	Glu	Glu 20	Val	Leu	Leu	Asp	Gly 25	Glu	Arg	Ile	Ser	Thr 30	Gly	Asn	
	Ser	Ser	Ile 35	Asp	Ile	Ser	Leu	Ser 40	Leu	Val	Gln	Phe	Leu 45	Val	Ser	Asn	

	Phe	Val 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp
5	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe 75	Leu	Val	Gln	Ile	Glu 80
	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile
10	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala
15	Phe	Lys	Glu 115	Trp	Glu	Val	Asp	Pro 120	Asn	Asn	Pro	Gly	Thr 125	Arg	Thr	Arg
13	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile
20	Pro 145	Ser	Phe	Arg	Ile	Ser 150	Gly	Phe	Glu	Val	Pro 155	Leu	Leu	Ser	Val	Tyr 160
	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170	Leu	Arg	Asp	Ser	Val 175	Ile
25	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
1.1 30	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Суѕ	Ala	Asn
•	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Lys	Ser 220	Thr	Tyr	Gln	Asp
	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile
40	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265	Val	Tyr	Thr	Asp	Pro 270	Leu	Ile
45	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
13	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
50	Asn 305	Asn	Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315	Val	Gly	Arg	Asn	Phe 320
	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser		Ile	Gly	Gly	Gly 335	

	Ile	Thr	Ser	Pro 340		туг	: Gly	' Arg	345		Asn	Gln	Glu	350		Arg
5	Ser	Phe	Thr 355		Asn	Gly	Pro	Val 360		Arg	Thr	Leu	Ser 365		Pro	Thr
	Leu	Arg 370		Leu	Gln	Gln	Pro 375	_	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
10	Gly 385		Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
15	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
-	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys 430	His	Ala
20 ប៊ា	Thr	Phe	Val 435	Gln	Arg	Ser	Gly	Thr 440	Pro	Phe	Leu	Thr	Thr 445	Gly	Val	Val
	Phe	Ser 450	Trp	Thr	His	Arg	Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro
25	Glu 465	Arg	Ile	Asn	Gln	Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
10 10	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe 490	Thr	Gly	Gly	Asp	Ile 495	Leu
13 (1)	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn
17 35 1-	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe	Arg	Tyr 525	Ala	Ser	Ser
	Arg	Asp 530	Ala	Arg	Val		Val 535	Leu	Thr	Gly	Ala	Ala 540	Ser	Thr	Gly	Val
40	Gly 545	Gly	Gln	Val -	Ser	Val 550	Asn	Met	Pro	Leu	Gln 555	Lys	Thr	Met	Glu	Ile 560
45	Gly	Glu	Asn		Thr 565	Ser	Arg	Thr	Phe	Arg 570	Tyr	Thr	Asp	Phe	Ser 575	Asn
	Pro	Phe	Ser	Phe 580	Arg	Ala	Asn	Pro	Asp 585	Ile	Ile	Gly	Ile	Ser 590	Glu	Gln
50	Pro	Leu	Phe 595	Gly	Ala	Gly	Ser	Ile 600	Ser	Ser	Gly		Leu 605	Tyr	Ile	Asp
	Lys	Ile 610	Glu	Ile	Ile		Ala 615	Asp	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp

	Leu 625	Glu	Arg	Ala	Gln	Lys 630	'Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
5	Gln	Ile	Gly	Leu	Lys 645	Thr	Asp	Val	Thr	Asp 650	Tyr	His	Ile	Asp	Gln 655	Val
	Ser	Asn	Leu	Val 660	Asp	Cys	Leu	Ser	Asp 665	Glu	Phe	Cys	Leu	Asp 670	Glu	Lys
10	Arg	Glu	Leu 675	Ser	Glu	Lys	Val	Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
15	Arg	Asn 690	Leu	Leu	Gln	Asp	Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
	Asp 705	Arg	Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	Asp 720
2 6	Asp	Val	Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp 735	Glu
u U	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745	Ile	Asp	Glu	Ser	Lys 750	Leu	Lys
25 1	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	Arg 760	Gly	Tyr	Ile	Glu	Asp 765	Ser	Gln	Asp
‡≟ 30	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn
L.P 774 C.R	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800
}≟ 35	Gly	Lys	Cys	Gly	Glu 805	Pro	Asn	Arg	Cys	Ala 810	Pro	His	Leu	Glu	Trp 815	Asn
	Pro	Asp	Leu	Asp 820	Суз	Ser	Cys	Arg	Asp 825	Gly	Glu	Lys	Cys	Ala 830	His	His
40	Ser	His	His 835	Phe	Thr	Leu	Asp	Ile 840	Asp	Val	Gly	Cys	Thr 845	Asp	Leu	Asn
45	Glu	Asp 850	Leu	Gly	Val	Trp	Val 855	Ile	Phe	Lys	Ile	860	Thr	Gln	Asp	Gly
	His 865	Ala	Arg	Leu	Gly	Asn 870	Leu	Glu	Phe	Leu	Glu 875	Glu	Lys	Pro	Leu	Leu 880
50	Gly	Glu	Ala	Leu	Ala 885	Arg	Val	Lys	Arg	Ala 890	Glu	Lys	Lys	Trp	Arg 895	Asp
	Lys	Arg	Glu	Lys 900	Leu	Gln	Leu	Glu	Thr 905	Asn	Ile	Val	Tyr	Lys 910	Glu	Ala

	Lys	GIU	915		. Asp) Ala	Leu	920		. AST	ser	Gln	925	_	Arg	, Leu
5	Gln	Val 930		Thr	Asn	Ile	Ala 935		Ile	His	Ala	Ala 940	-	Lys	Arg	Val
	His 945		Ile	Arg	Glu	Ala 950	_	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960
10	Val	Asn	Ala	Ala	Ile 965		Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala
15	Tyr	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn
	Asn	Gly	Leu 995	Leu	Cys	Trp	Asn	Val	_	Gly	His	Val	Asp 100		Glu	Glu
20	Gln	Asn 1010		His	Arg	Ser	Val 1019		Val	Ile	Pro	Glu 1020	_	Glu	Ala	Glu
	Val 1025		Gln	Glu	Val	Arg 1030		Cys	Pro	Gly	Arg 1035		Tyr	Ile	Leu	Arg 1040
2 \$	Val	Thr	Ala	Tyr	Lys 1045		Gly	Tyr	Gly	Glu 1050	_	Cys	Val	Thr	Ile 1055	
± 30	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 1065	-	Phe	Ser	Asn	Cys 1070		Glu
C) IN	Glu	Glu	Val 1075		Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 1085	_	Thr	Gly
35 35	Thr	Gln 1090		Glu	Tyr	Glu	Gly 1095		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr
	Asp 1105		Ala	Tyr	_	Asn 1110		Pro	Ser		Pro 1115		Asp	Tyr	Ala	Ser 1120
40	Val	Tyr	Glu	Glu	Lys 1125		Tyr	Thr	Asp	Gly 1130	_	Arg	Glu	Asn	Pro 1135	-
45	Glu	Ser	Asn	Arg 1140	_	Tyr	Gly	Asp	Tyr 1145		Pro	Leu	Pro	Ala 1150	_	Tyr
	Val	Thr	Lys 1155	_	Leu	Glu	Tyr	Phe 1160		Glu	Thr	Asp	Lys 1165		Trp	Ile
50	Glu	Ile 1170	_	Glu	Thr	Glu	Gly 1175		Phe	Ile	Val	Asp 1180		Val	Glu	Leu
	Leu 1185		Met	Glu	Glu											

5	(i	(; (;	QUEN A) L B) T C) S'	ENGT YPE : TRAN	H: 3! nuc: DEDNI	567 leic ESS:	base aci sin	pai: d	rs					
10	(ix	(2	ATURI A) Ni B) L	AME/			3567							
15	(xi)) SE(QUEN	CE DI	ESCRI	(PTIC	ON: S	SEQ I	ID NO	0:11	:			
								TGC Cys						48
10 10 120								GGA Gly 25						96
								CTT Leu						144
£								GTT Val						192
50 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1								GAT Asp						240
								GAA Glu						288
40								AAT Asn 105						3-36
45								CAT His						384
50		Asp						GAT Asp						432
	Ser					Gly		GAA Glu			Leu			480

(2) INFORMATION FOR SEQ ID NO:11:

				Leu			Leu			ATT	528
5								AAT Asn			576
		_	180			185			190	-	
10								CAC His 205			624
15								ACG Thr			672
20 口								TTG Leu			720
10 10 15								AGA Arg			768
The city was proceed to the time.								GAC Asp			816
30 mm m								CCT Pro 285			864
3	_			Ala				TTT Phe			912
40								GGA Gly			960
45								GGA Gly			1008
70								GAG Glu			1056
50								TCA Ser 365			1104

	TTA Leu	CGA Arg 370	TTA Leu	TTA Leu	CAG Gln	CAÁ Gln	Pro 375	TGG Trp	CCA Pro	GCG Ala	CCA Pro	CCA Pro 380	TTT Phe	AAT Asn	TTA Leu	CGT Arg	1152
5													AGC Ser				1200
10	CGA Arg	GGA Gly	AGA Arg	GGT Gly	ACG Thr 405	GTT Val	GAT Asp	TCT Ser	TTA Leu	ACT Thr 410	GAA Glu	TTA Leu	CCG Pro	CCT Pro	GAG Glu 415	GAT Asp	1248
.15													TTA Leu				1296
20													ACT Thr 445				1344
20 () () ()													ACA Thr				1392
25 14 14													AGA Arg				1440
30 3	GGC Gly	ACC Thr	TCT Ser	GTC Val	ATT Ile 485	ACA Thr	GGA Gly	CCA Pro	GGA Gly	TTT Phe 490	ACA Thr	GGA Gly	GGG Gly	GAT Asp	ATC Ile 495	CTT Leu	1488
17 17 175													GTC Val				1536
	TCA Ser	CCA Pro	ATT Ile 515	ACC Thr	CAA Gln	AGA Arg	TAC Tyr	CGT Arg 520	TTA Leu	AGA Arg	TTT Phe	CGT Arg	TAC Tyr 525	GCT Ala	TCC Ser	AGT Ser	1584
40	AGG Arg	GAT Asp 530	GCA Ala	CGA Arg	GTT Val	ATA Ile	GTA Val 535	TTA Leu	ACA Thr	GGA Gly	GCG Ala	GCA Ala 540	TCC Ser	ACA Thr	GGA Gly	GTG Val	1632
45	GGA Gly 545	Gly	CAA Gln	GTT Val	AGT Ser	GTA Val 550	AAT Asn	ATG Met	CCT Pro	CTT Leu	CAG Gln 555	AAA Lys	ACT Thr	ATG Met	GAA Glu	ATA Ile 560	1680
50	GGG Gly	GAG Glu	AAC Asn	TTA Leu	ACA Thr 565	Ser	AGA Arg	ACA Thr	TTT	AGA Arg 570	Tyr	ACC Thr	GAT Asp	TTT Phe	AGT Ser 575	AAT Asn	1728

				Arg				Ile			Glu	CAA Gln	1776
5		TTT Phe 595								Tyr			1824
10		GAA Glu											1872
15		AGA Arg											1920
20		GGG Gly											1968
Ö		TTA Leu											2016
13 13 13 25 13 14 14 14 14 14 14 14 14 14 14 14 14 14		TTG Leu 675											2064
130 130		TTA Leu			Asp								2112
() () () () ()		GGC Gly											2160
40		TTC Phe	Lys										2208
		CCA Pro					Gln						2256
45		ACC Thr 755				Leu							2304
50		ATC Ile			Ile .								2352

	 		TCC Ser 790			Ala		ATC Ile 800	2400
5			CCG Pro						2448
10			TCC Ser						2496
15			TTG Leu						2544
20			TGG Trp						2592
5 10 10 125			AAT Asn 870						2640
25 			CGT Arg						2688
			CAG Gln						2736
5 135 14			GCT Ala						2784
40			ATC Ile						2832
40			GCG Ala 950						2880
45			TTC Phe						2928
50			GCG Ala						2976

			Leu					Lys					Val		GAG Glu	3024
5	AAC Asn 101	Asn					Leu					Trp			GAA Glu	3072
10	TCA Ser 5					Val					Gly					3120
15	ACA Thr				Glu					Gly					His	3168
20	ATC Ile			Asn					Lys					Val		3216
	GAA Glu		Tyr					Val					Tyr			3264
25 14 14 14 14 14 14 14 14 14 14 14 14 14	CAA Gln 1090	Glu					Thr					Asn				3312
<u>30</u>	GAA Glu					Asn					Ala					3360
	TAT Tyr				Ser					Arg					Cys	3408
40	TCT Ser			Gly					Thr					Gly		3456
10	ACA Thr		Asp					Pro					Val			3504
45	ATC Ile 1170	Gly					Thr					Ser			TTA Leu-	3552
50	CTT Leu															3567

⁽²⁾ INFORMATION FOR SEQ ID NO:12:

			(i)	SEQ	UENC:	E CH	ARAC'	TERI:	STIC	S:						
				()	A) L	ENGT	H: 1	189 a	amino		ids					
5								line								
			(ii)	MOLI	ECULI	TY!	?E: p	prote	ein							
10			(xi)	SEQU	ENCE	E DES	CRIE	PTION	I: SE	EQ II	NO:	12:				
	Met 1		ı Glu	Asn	Asn S		Asn	Gln	Cys	Ile 10		Tyr	Asn	Cys	Leu 15	Ser
15	Asn	Pro	Glu	Glu 20		Leu	Leu	Asp	Gly 25		Arg	Ile	Ser	Thr 30		Asn
	Ser	Ser	Ile 35	Asp	Ile	Ser	Leu	Ser 40	Leu	Val	Gln	Phe	Leu 45	Val	Ser	Asn
20 []	Phe	Val 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp
	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe 75	Leu	Val	Gln	Ile	Glu 80
in of maje perm left of the fire per cultur p ¹ worth	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile
30	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala
	Phe	Lys	Glu 115	Trp	Glu	Glu	Asp	Pro 120	His	Asn	Pro	Ala	Thr 125	Arg	Thr	Arg
55	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile
40	Pro 145	Ser	Phe	Arg	Ile	Ser 150	Gly	Phe	Glu	Val	Pro 155	Leu	Leu	Ser	Val	Tyr 160
	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170	Leu	Arg	Asp	Ser	Val 175	Ile
45	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Суѕ	Ala	Asn
50	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Lys	Ser 220	Thr	Tyr	Gln	Asp
	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240

	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250		Arg	Arg	Tyr	Pro 255	Ile
5	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265		туr	Thr	Asp	Pro 270	Leu	Ile
10	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
. 15	Asn 305	Asn	Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315	Val	Gly	Arg	Asn	Phe 320
	Tyr	Trp	Gly	Gly	His 325	Arg	Val	Ile	Ser	Ser 330	Leu	Ile	Gly	Gly	Gly 335	Asn
20 .0 .0	Ile	Thr	Ser	Pro 340	Ile	Tyr	Gly	Arg	Glu 345	Ala	Asn	Gln	Glu	Pro 350	Pro	Arg
74 74 25	Ser	Phe	Thr 355	Phe	Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365	Asn	Pro	Thr
Here Here H	Leu	Arg 370	Leu	Leu	Gln	Gln	Pro 375	Trp	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
14 10	Gly 385	Val	Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
<u>1</u>	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys 430	His	Ala
40	Thr	Phe	Val 435	Gln	Arg	Ser	Gly	Thr 440	Pro	Phe	Leu	Thr	Thr 445	Gly	Val	Val
	Phe	Ser 450	Trp	Thr	His	Arg	Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro
45	Glu 465	Arg	Ile	Asn	Gln	Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe 490	Thr	Gly	Gly	Asp	Ile 495	Leu
50	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn
	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg		Arg	Phe	Arg	Tyr		Ser	Ser

	Arg	Asp 530		Arg	Val	Ile	Val 535		Thr	Gly	Ala	Ala 540		Thr	Gly	Va:
5	Gly 545		Gln	Val	Ser	Val 550		Met	Pro	Leu	Gln 555	Lys	Thr	Met	Glu	11e 560
10	Gly	Glu	Asn	Leu	Thr 565	Ser	Arg	Thr	Phe	Arg 570	Tyr	Thr	Asp	Phe	Ser 575	Asr
	Pro	Phe	Ser	Phe 580	Arg	Ala	Asn	Pro	Asp 585	Ile	Ile	Gly	Ile	Ser 590	Glu	Gln
15	Pro	Leu	Phe 595	Gly	Ala	Gly	Ser	Ile 600	Ser	Ser	Gly	Glu	Leu 605	Tyr	Ile	Asp
· •	Lys	Ile 610	Glu	Ile	Ile	Leu	Ala 615	Asp	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp
2 0 □	Leu 625	Glu	Arg	Ala	Gln	630	Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
↓ 1 25	Gln	Ile	Gly	Leu	Lys 645	Thr	Asp	Val	Thr	Asp 650	Tyr	His	Ile	Asp	Gln 655	Va1
	Ser	Asn	Leu	Val 660	Asp	Cys	Leu	Ser	Asp 665	Glu	Phe	Cys	Leu	Asp 670	Glu	Lys
30 3	Arg	Glu	Leu 675	Ser	Glu	Lys	Val	Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
# # #	Arg	Asn 690	Leu	Leu	Gln	Asp	Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
35	Asp 705	Arg	Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	Asp 720
40	Asp	Val	Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp 735	Glu
	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745	Ile	Asp	Glu	Ser	Lys 750	Leu	Lys
45	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	Arg 760	Gly	Tyr	Ile	Glu	Asp 765	Ser	Gln	Asp
	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn
50	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800
	Gly	Lys	Cys	Gly	Glu 805	Pro	Asn	Arg	Сув	Ala 810	Pro	His	Leu	Glu	Trp 815	Asn

	Pro	Asp	Leu	Asp 820	_	Ser	Cys	Arg	Asp 825		Glu	Lys	Cys	Ala 830		His
5	Ser	His	His 835	Phe	Thr	Leu	Asp	Ile 840	Asp	Val	Gly	Cys	Thr 845	Asp	Leu	Asn
10	Glu	Asp 850	Leu	Gly	Val	Trp	Val 855	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly
10	His 865	Ala	Arg	Leu	Gly	Asn 870	Leu	Glu	Phe	Leu	Glu 875	Glu	Lys	Pro	Leu	Leu 880
15	Gly	Glu	Ala	Leu	Ala 885	Arg	Val	Lys	Arg	Ala 890	Glu	Lys	Lys	Trp	Arg 895	Asp
	Lys	Arg	Glu	Lys 900	Leu	Gln	Leu	Glu	Thr 905	Asn	Ile	Val	Tyr	Lys 910	Glu	Ala
20 0	Lys	Glu	Ser 915	Val	Asp	Ala	Leu	Phe 920	Val	Asn	Ser	Gln	Tyr 925	Asp	Arg	Leu
道 划 型5	Gln	Val 930	Asp	Thr	Asn	Ile	Ala 935	Met	Ile	His	Ala	Ala 940	Asp	Lys	Arg	Val
THE THE	His 945	Arg	Ile	Arg	Glu	Ala 950	Tyr	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960
‡30 £3	Val	Asn	Ala	Ala	Ile 965	Phe	Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala
	Tyr	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn
<u> </u>	Asn	Gly	Leu 995	Leu	Cys	Trp	Asn	Val 1000	-	Gly	His	Val	Asp 1005		Glu	Glu
40	Gln	Asn 1010		His	Arg	Ser	Val 1015	Leu	Val	Ile	Pro	Glu 1020		Glu	Ala	Glu
	Val 1025		Gln	Glu	Val	Arg 1030		Cys	Pro	Gly	Arg 1035		Tyr	Ile	Leu	Arg 1040
45	Val	Thr	Ala	Tyr	Lys 1045		Gly:	Tyr	Gly	Glu 1050		Суз	Val	Thr	Ile 1055	
	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 1065	_	Phe	Ser	Asn	Cys 1070		Glu
50	Glu	Glu	Val 1075	_	Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 1085		Thr	Gly
	Thr	Gln 1090		Glu	Tyr	Glu	Gly 1099	Thr	Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr

	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser 1105 1110 1115 1120	
5	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys 1125 1130 1135	
10	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr 1140 1145 1150	
10	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile 1155 1160 1165	
15	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170 1175 1180	
	Leu Leu Met Glu Glu 1185	
20 (3 (3	(2) INFORMATION FOR SEQ ID NO:13: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
30 	GCATTTAAAG AATGGGAAGA AGATAATAAT CCAGCAACCA GGACCAGAG	49
35	(2) INFORMATION FOR SEQ ID NO:14:	
 - 4 40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 55 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
45	GCATTTAAAG AATGGGAAGA AGATCCTAAT GCAAATCCAG CAACCAGGAC CAGAG	55
	(2) INFORMATION FOR SEQ ID NO:15:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
j	CCCGATCGGC CGCATGC	17
	(2) INFORMATION FOR SEQ ID NO:16:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
	GCATTTAAAG AATGGGAAGG GATCCTAGGA ATCCAGCAAC CAGGACCAGA G	51
	(2) INFORMATION FOR SEQ ID NO:17:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
	GAGCTCTTGT TAAAAAAGGT GTTCCAGATC	30
	(2) INFORMATION FOR SEQ ID NO:18:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	<pre>(ix) FEATURE: (A) NAME/KEY: modified_base (B) LOCATION: 1939 (D) OTHER INFORMATION: /note= "N = G, A, T or C"</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
	GCATTTAAAG AATGGGAANN NNNNNNNNN NNNNNNNNA CCAGGACCAG AGTAATTGAT	60
	CG	62

(2) INFORMATION FOR SEQ ID NO:19:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 55 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
10	GGGCTACTTG AAAGGGACAT TCCTTCGTTT GCAATTTCTG GATTTGAAGT ACCCC	55
	(2) INFORMATION FOR SEQ ID NO:20:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 39 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20 ᠿ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
ū	CCAAGAAAAT ACTAGAGCTC TTGTTAAAAA AGGTGTTCC	39
ñ		
4		
000 75	(2) INFORMATION FOR SEQ ID NO:21:	
; \;	(i) SEQUENCE CHARACTERISTICS:	
i Fi	(A) LENGTH: 50 base pairs	
	(B) TYPE: nucleic acid	
ร็ด	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
IJ	(5) 102020021 220022	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
ĻT	(XI) SEQUENCE BESCRIFTION: SEQ IS 100.00	
	GAGATTCTGT AATTTTTGGA GAAGCATGGG GGTTGACAAC GATAAATGTC	50
	(2) INFORMATION FOR SEQ ID NO:22:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 63 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
	GCATTTAAAG AATGGGAAGA AGATCCTAAT AATCCAGCAA CCAGGACCAG AGTAATTGAT	60
.		63
50	CGC	Ų
	(2) INFORMATION FOR SEQ ID NO:23:	
	(2) INFORMATION FOR SEQ ID NO.23.	

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 7 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(wi) CROMENCE DECORPORTON GEO ID NO 22	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
	Glu Asp Pro Asn Asn Pro Ala	
10	1 5	
	(2) INFORMATION FOR SEQ ID NO:24:	
15	(i) CEOUTINGE OVER COURT OF	
13	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 51 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
20 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
H A		
	GCATTTAAAG AATGGGAAGG GATCCTAGGA ATCCAGCAAC CAGGACCAGA G	51
`4 'U_		
25		
ų.	(2) INFORMATION FOR SEQ ID NO:25:	
F	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 63 base pairs	
3 0	(B) TYPE: nucleic acid	
3	(C) STRANDEDNESS: single	
-	(D) TOPOLOGY: linear	
F	(b) Toronogi. Timeat	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
J	GCATTTAAAG AATGGGAAGA TGATCCTCAT AATCCCACAA CCAGGACCAG AGTAATTGAT	60
	CGC	63
40		
+0	(2) INFORMATION FOR SEC ID NO. 26.	
	(2) INFORMATION FOR SEQ ID NO:26:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 7 amino acids	
45	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(with appropriate programmers and the second	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
J U	New New Date New Date Mha	
	Asp Asp Pro His Asn Pro Thr	
	1 3	

	(2)	INF	ORMA	TION	FOR	SEC	ř ID	NO : 2	7:								
5		(i	() (1 ()	A) L 3) T C) S'	ENGT YPE : TRAN	H: 7 ami DEDN	ami no a	sing	cids								
10								ON: S		ID NO	0:27:	:					
		1				5											
15	(2)	INFC	RMAT	'ION	FOR	SEQ	ID N	IO : 28	:								
		(i)	(A (B (C) LE) TY) ST	NGTH PE: RAND	: 50 amin EDNE	ami o ac	sing	cids								
		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:28:						
25 17		Thr 1	Asn	Pro	Ala	Leu 5	Arg	Glu	Glu	Met	Arg 10	Ile	Gln	Phe	Asn	Asp 15	Met
: :4 :3 0		Asn	Ser	Ala	Leu 20	Thr	Thr	Ala	Ile	Pro 25	Leu	Leu	Ala	Val	Gln 30	Asn	Tyr
ā m		Gln	Val	Pro 35	Leu	Leu	Ser	Val	Tyr 40	Val	Gln	Ala	Ala	Asn 45	Leu	His	Leu
35		Ser	Val 50														
	(2) I	NFOR	ITAMS	ON E	FOR S	SEQ :	ID NO	0:29:	:								
40 45		(i)	(A) (B) (C)	LEN TYP STF	IGTH PE: 8 RANDI	: 50 amino EDNES	amir	singl	cids								
	(xi)	SEQU	ENCE	DES	CRI	PTION	N: SE	Q II	NO:	29:						
50		Thr 1	Asn	Pro	Ala	Leu 5	Thr	Glu	Glu	Met	Arg 10	Ile	Gln	Phe	Asn	Asp 15	Met
		Asn	Ser	Ala	Leu 20	Thr	Thr	Ala	Ile	Pro 25	Leu	Phe	Thr	Val	Gln 30	Asn	Tyr

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu 40 Ser Val 5 50 (2) INFORMATION FOR SEQ ID NO:30: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met 5 10 15 20 0 0 1 1 25 Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Ala Val Gln Asn Tyr 20 25 Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu 40 1-1 *... Ser Val IN 50 (2) INFORMATION FOR SEQ ID NO:31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid . (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31: 40 Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met 5 10 Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Thr Val Gln Asn Tyr 45 20 Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Val Asn Leu His Leu 35 40 50 Ser Val 50

(2) INFORMATION FOR SEQ ID NO:32:

5		(1)	(A (B (C	L) LE S) TY C) ST	NGTH PE: RAND	: 50 amin EDNE GY:	ami o ac SS:	ino a cid sing	cids	3							
		(xi)	SEQ	UENC	E DE	SCRI	PTIC	N: S	EQ I	D NO	:32:						
10		Thr 1	Asn	Pro	Ala	Leu 5	Arg	Glu	Glu	Met	Arg 10	Ile	Gln	Phe	Asn	Asp 15	Met
15		Asn	Ser	Ala	Leu 20	Thr	Thr	Ala	Ile	Pro 25	Leu	Phe	Ala	Val	Gln 30	Asn	Tyr
		Gln	Val	Pro 35	Leu	Leu	Ser	Val	Tyr 40	Val	Gln	Ala	Ala	Asn 45	Leu	His	Leu
20 ©		Ser	Val 50		•									ē			
0	(2)	INFO	RMATI	ION E	FOR S	SEQ I	D NO	0:33	:								
00078475 2 0054		(i)	(A) (B)	LEN TYE STR	IGTH: PE: a PANDE	ARACT 50 mino DNES Y: 1	amir aci S: s	no ad id singl	cids								
		(xi)	SEQU	JENCE	DES	CRIP	TION	1: SE	EQ II	NO:	33:						
13 35		Asn 1	Asn	Ala	Gln	Leu 5	Arg	Glu	Asp	Val	Arg 10	Ile	Arg	Phe	Ala	Asn 15	Thr
þ .l.		Asp	Ąsp	Ala	Leu 20	Ile	Thr	Ala	Ile	Asn 25	Asn	Phe	Thr	Leu	Thr 30	Ser	Phe
40		Glu	Ile	Pro 35	Leu	Leu	Ser	Val	Tyr 40	Val	Gln	Ala	Ala	Asn 45	Leu	His	Leu
		Ser	Leu 50	•													
45	(2)	INFOR	ITAM	ON F	or s	EQ I	D.NC):34:	:								
50		(i)	(A) (B) (C)	LEN TYP STR	IGTH: PE: a LANDE	RACT 50 mino DNES Y: 1	amin aci S: s	o ad d singl	cids								
		(xi)	SEQU	JENCE	DES	CRIP	TION	1: SE	EQ II	NO:	34:						

(i) SEQUENCE CHARACTERISTICS:

		As 1	n Asn	Ala	GIn	Leu 5	Arg	Glu	ı As	p Va	1 Ar	g Ile	Ar	g Phe	∋ Ala	Asr 15	Thi
5		As	p Asp	Ala	Leu 20	Ile	Thr	Ala	a Il	e Ası 25	n Ası	n Phe	Thi	r Lei	Thr	Ser	Phe
10		Glı	u Ile	Pro 35	Leu	Leu	Ser	Val	. Ty:	r Val	l Glr	ı Ala	Ala	Asn 45	. Leu	His	Leu
		Sei	t Leu 50														
- 15	(2)	INFO	RMATI	ON F	OR S	SEQ 1	D NO):35	:								
20 13 13 13 13 13 13 13 13 13 13 13 13 13 1		(i)	(B) (C)	LEN TYP STR	GTH: E: a ANDE	50 mino DNES	ERIS amin aci S: s inea	o ao d ingl	cids								
10		(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	EQ I	D NO	:35:					•	
25 - -		Asn 1	Asn 1	Pro 1		Ser 5	Gln	Glu	Arg	Val	Arg 10	Thr	Arg	Phe	Arg	Leu 15	Thr
1.Ti		Asp	Asp A		Ile ' 20	Val '	Thr	Gly	Leu	Pro 25	Thr	Leu	Ala	Ile	Arg 30	Asn	Leu
		Glu	Val V	/al / 35	Asn 1	Leu :	Ser '	Val	Tyr 40	Thr	Gln	Ala	Ala	Asn 45	Leu	His	Leu
35		Ser	Leu 50														
	(2)	INFOR	RMATIC	N FC	OR SI	EQ II	ON C	: 36 :									
40 45		(i)	(B) (C)	LENG TYPE STRA	TH: E: an ANDEI	50 a mino ONESS	ERIST amino acio S: si inear	o ac i ingl	ids								
.5		(xi)	SEQUE	ENCE	DESC	CRIPT	rion:	SE	Q II	NO:	36:						
50		Asn 1	Asn P	ro G	lu 1		Arg 1	Thr .	Arg	Val	Ile 10	Asp .	Arg	Phe	_	Ile : 15	Leu
		Asp	Gly I		eu (3lu A	Arg A	4sp	Ile	Pro 25	Ser	Phe .	Arg		Ser	Gly	Phe

			-	35					40					45			, Deu
5		Ala	11e 50	•													
	(2)	INFO	RMAT	'ION	FOR	SEQ	ID N	10:37	':								
10		(i)	(A (B (C) LE) TY) ST	NGTH PE: RAND	: 50 amin EDNE	TERI ami o ac SS: line	no a id sing	cids								
		(xi)	SEQ	UENC	E DE	SCRI	PTIO:	N: S	EQ I	D NO	:37:						
20		Asp 1	Asn	Pro	Val	Thr 5	Arg	Thr	Arg	Val	Val 10	Asp	Arg	Phe	Arg	Ile 15	Leu
20 21 11 11 11 12 15 15 15 15 15 15 15 15 15 15 15 15 15		Asp	Gly	Leu	Leu 20	Glu	Arg	Asp	Ile	Pro 25	Ser	Phe	Arg	Ile	Ala 30	Gly	Phe
25		Glu	Val	Pro 35	Leu	Leu	Ser	Val	Tyr 40	Ala	Gln	Ala	Ala	Asn 45	Leu	His	Leu
A Trans		Ala	Ile 50														
1 3 0 []	(2)	INFO	RMAT	ON I	FOR S	SEQ 1	D NO	0:38:	:								
130 C C C C C C C C C C C C C C C C C C C		(i)	(B)	LEN TYP STR	NGTH: PE: 8 RANDE	50 minc EDNES	TERIS amir aci SS: sinea	no ad id singl	ids							**	
40		(xi)	SEQU	JENCE	E DES	CRIE	OITS	1: SE	EQ II	NO:	38:						
		Thr 1	Asn	Pro	Ala	Leu 5	Lys	Glu	Glu	Met	Arg 10	Thr	Gln	Phe	Asn	Asp 15	Met
45		Asn	Ser	Ile	Leu 20	Val	Thr	Ala	Ile	Pro 25	Leu	Phe	Ser	Val	Gln 30	Asn	Tyr
		Gln	Val	Pro 35	Phe	Leu	Ser	Val	Tyr 40	Val	Gln	Ala	Ala	Asn 45	Leu	His	Leu
50		Ser	Val 50														

Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu

(2) INFORMATION FOR SEQ ID NO:39:

Glu Ile Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn Leu His Leu 40 Ser Leu 5 50 (2) INFORMATION FOR SEQ ID NO:44: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44: Asp Asn Glu Ala Ala Lys Ser Arg Val Ile Asp Arg Phe Arg Ile Leu 5 20 0 10 Asp Gly Leu Ile Glu Ala Asn Ile Pro Ser Phe Arg Ile Ile Gly Phe 25 ſŪ Glu Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu 25 40 7.4 Į Ala Leu ₽ 50 }≟ 30 (2) INFORMATION FOR SEQ ID NO:45: I C (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: 40 Asp Asn Thr Ala Ala Arg Ser Arg Val Thr Glu Arg Phe Arg Ile Ile 1 5 Asp Ala Gln Ile Glu Ala Asn Ile Pro Ser Phe Arg Ile Pro Gly Phe 45 20 25 Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu 40 45 50 Ala Leu 50

(2) INFORMATION FOR SEQ ID NO:46:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid- (C) STRANDEDNESS: single (D) TOPOLOGY: linear 														
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:														
10	Asp Asp Ala Arg Thr Arg Ser Val Leu Tyr Thr Gln Tyr Ile Ala Leu 1 5 10 15														
. 15	Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn Gln 20 25 30														
	Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu 35 40 45														
20	Leu Leu 50														
*==	(2) INFORMATION FOR SEQ ID NO:47:														
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear														
ā	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:														
17 13 35	Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu 1 5 10 15														
	Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu 20 25 30														
40	Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu 35 40 45														
	Leu Leu 50														
45	(2) INFORMATION FOR SEQ ID NO:48:														
	(i) SEQUENCE CHARACTERISTICS:														
50	(A) LENGTH: 50 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear														
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:														

		1	. ASP	Ala	Arg	5	Arg	361	116	116	10	GIU	Arg	lyr	vai	15	. Let
5		Glu	. Leu	Asp	Ile 20	Thr	Thr	Ala	Ile	Pro 25	Leu	Phe	Arg	Ile	Arg 30	Asn	Glu
10		Glu	Val	Pro 35	Leu	Leu	Met	Val	Tyr 40	Ala	Gln	Ala	Ala	Asn 45	Leu	His	Lev
10		Leu	Leu 50														
15	(2)	INFO	RMAT:	ION E	FOR S	SEQ :	ID NO	0:49	:								
			(A) (B) (C) (D)	UENCE) LEN) TYF) STR) TOF	IGTH: PE: & RANDI POLOC	: 50 amino EDNES GY: 3	amir o aci SS: s linea	no ad id sing: ar	cids le								
4.		(xi)	SEQ	JENCE	DES	CRI	OITS	I: SI	EQ II	NO:	49:						
75 }≟ `J		Asn 1	Asp	Ala	Arg	Ser 5	Arg	Ser	Ile	Ile	Arg 10	Glu	Arg	Tyr	Ile	Ala 15	Leu
ļN		Glu	Leu	Asp	Ile 20	Thr	Thr	Ala	Ile	Pro 25	Leu	Phe	Ser	Ile	Arg 30	Asn	Glu
		Glu	Val	Pro 35	Leu	Leu	Met	Val	Tyr 40	Ala	Gln	Ala	Ala	Asn 45	Leu	His	Leu
5		Leu	Leu 50														
	(2)	INFOR	ITAMS	ON F	OR S	EQ I	D NC	:50:									
10 15		(i)	(A) (B) (C)	JENCE LEN TYP STR TOP	GTH: E: a ANDE	50 minc DNES	amin aci S: s	o ac .d :ingl	ids								
IJ		(xi)	SEQU	JENCE	DES	CRIE	MOIT	I: SE	EQ II	NO:	50:						
50		Asn 1	Asn	Thr	Arg	Ala 5	Arg	Ser	Val	Val	Lys 10	Ser	Gln	Tyr	Ile	Ala 15	Leu
, 0		Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe	Ala	Val	Ser	Gly	Glu

```
40
           Leu Leu
  5
               50
      (2) INFORMATION FOR SEQ ID NO:51:
10
           (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 50 amino acids
                 (B) TYPE: amino acid
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear
15
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
           Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn Gln Tyr Ile Ala Leu
                           5
                                                10
20
           Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe Ala Val Ser Gly Glu
Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala Asa Leu His Leu
                                       40
           Leu Leu
              50
30
10
10
      (2) INFORMATION FOR SEQ ID NO:52:
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 22 base pairs
33
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
40
     GGATCCCTCG AGCTGCAGGA GC
                                                                              22
      (2) INFORMATION FOR SEQ ID NO:53:
45
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 55 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
50
                (D) TOPOLOGY: linear
          (ix) FEATURE:
                (A) NAME/KEY: modified base
                (B) LOCATION: 31..33
```

Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala Asa Leu His Leu

	(D) OTHER INFORMATION: /note= "N = C, A, T or G"	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
5	GGGCTACTTG AAAGGGACAT TCCTTCGTTT NNNATTTCTG GATTTGAAGT ACCCC	55
	(2) INFORMATION FOR SEQ ID NO:54:	
10 15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
	GCATTTAAAG AATGGGAAGT AGATCCTAAT AATCCTGGAA CCAGGACCAG AGTAATTGAT	60
20 []	CGC	63
12	(2) INFORMATION FOR SEQ ID NO:55:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear 	
₹ <u>0</u> (3	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
	Val Asp Pro Asn Asn Pro Gly 1 5	
	(2) INFORMATION FOR SEQ ID NO:56:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	-
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
	GCATTTAAAG AATGGGAAGA AGATCCCCAT AATCCAGCAA CCAGGACCAG AGTAATTGAT	60
50	CGC	63
	(2) INFORMATION FOR SEQ ID NO:57:	

(i) SEQUENCE CHARACTERISTICS:

					TYPE:				icius	•							
			((C) S	TRAN	IDEDN	TESS:										
5			((D) I	COPOL	.OGY :	lin	ear									
3		(xi	.) SE	QUEN	ICE D	ESCR	IPTI	ON:	SEQ	ID N	O:57	':					
		Gl	u As	p Pr	o Hi	s As	n Pr	o Al	.a								
• •		1		-		5											
10																	
	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 5	8:								
		.(i) SE	QUEN	CE C	HARA	CTER	ISTI	CS:								
15					ENGT				_	rs							
					YPE: TRAN												
					OPOL				_								
20		(ix) FF.	ATUR:	F .												
20 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		(170			ame/i	KEY:	CDS										
.A			(1	B) L	OCAT:	ION:	1	3567									
*# *!		(xi) SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ :	ID N	0:58	:					
125																	
ļė 1					AAT Asn												48
	1	Giu	GIU	ASII	5	GIII	ASII	GIII	Cys	10	FIO	171	ASII	Cys	15	561	
ē								~							~~~		0.5
<u> </u>					GTA Val												96
				20					25		5			30	1		
5 5 5	TC A	TC A	» mm	CAT	N CCCC	TOT	CTC	TC N	CCC	C TOTT	CAC	mmm.	CTC	CTA	TOT.	እ አ C	144
5 5					ATT Ile												777
; =			· 35	-				40					45				
	ጥጥጥ	СТА	CCA	GGG	GGA	GGA	ئابىل ىك	тта	GTT	GGA	ATT	АТА	GAT	ттт	GTA	TGG	192
					Gly												
40		50					55					60					
	GGA	ATA	GTT	- GGC	CCT	TCT	CAA	TGG	GAT	GCA	TTT	CTA	GTA	CAA	ATT	GAA	240
	Gly	Ile	Val	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile		
45	65					70					75					80	
73	CAA	TTA	ATT	AAT	GAA	AGA	ATA	GCT	GAA	TTT	GCT	AGG	AAT	GCT	GCT	ATT	288
	Gln	Leu	Ile	Asn	Glu	Arg	Ile	Ala	Glu		Ala	Arg	Asn	Ala		Ile	
					85					90					95		
50	GCT	AAT	TTA	GAA	GGA	TTA	GGA	AAC	AAT	TTC	AAT	ATA	TAT	GTG	GAA	GCA	336
	Ala	Asn	Leu		Gly	Leu	Gly	Asn		Phe	Asn	Ile	Tyr		Glu	Ala	
				100					105					110			

(A) LENGTH: 7 amino acids

		TTT	AAA	GAA	TGG	GAA	GAA	GAT	CCT	AAT	AAT	CCA	GCA	ACC	AGG	ACC	AGA	384
		Phe	Lys	Glu	Trp	Glu	Glu	Asp	Pro	Asn	Asn	Pro	Ala	Thr	Arg	Thr	Arg	
			•	115	_			_	120					125	_		•	
	5	GTA	ATT	GAT	CGC	TTT	CGT	ATA	CTT	GAT	GGG	CTA	CTT	GAA	AGG	GAC	ATT	432
		Val	Ile	Asp	Arg	Phe	Arg	Ile	Leu	Asp	Gly	Leu	Leu	Glu	Arg	Asp	Ile	
			130	•	_		•	135		•	•		140		_	•		
		CCT	TCG	TTT	GCA	ATT	TCT	GGA	TTT	GAA	GTA	CCC	CTT	TTA	TCC	GTT	TAT	480
	10	Pro	Ser	Phe	Ala	Ile	Ser	Gly	Phe	Glu	Val	Pro	Leu	Leu	Ser	Val	Tyr	
		145					150	•				155					160	
		GCT	CAA	GCG	GCC	AAT	CTG	CAT	CTA	GCT	ATA	TTA	AGA	GAT	TCT	GTA	ATT	528
		Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Ala	Ile	Leu	Arq	Asp	Ser	Val	Ile	
	15					165					170		_	-		175		
		TTT	GGA	GAA	AGA	TGG	GGA	TTG	ACA	ACG	ATA	AAT	GTC	AAT	GAA	AAC	TAT	576
		Phe	Gly	Glu	Arq	Trp	Gly	Leu	Thr	Thr	Ile	Asn	Val	Asn	Glu	Asn	Tyr	
			•		180	-	-			185					190		•	
	20																	
	r r	AAT	AGA	CTA	ATT	AGG	CAT	ATT	GAT	GAA	TAT	GCT	GAT	CAC	TGT	GCA	AAT	624
	١ <u></u>	Asn	Arg	Leu	Ile	Arg	His	Ile	Asp	Glu	Tyr	Ala	Asp	His	Cys	Ala	Asn	
	₹Ū		_	195		_			200		-		-	205	-			
	₹ <u>0</u> *4																	
	25	ACG	TAT	AAT	CGG	GGA	TTA	AAT	AAT	TTA	CCG	GCT	AGC	ACG	TAT	CAA	GAT	672
	ļ.d.	Thr	Tyr	Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Ala	Ser	Thr	Tyr	Gln	Asp	
	14		210		_	_		215					220		_		_	
	ĮÑ.																	
		TGG	ATA	ACA	TAT	AAT	CGA	TTA	CGG	AGA	GAC	TTA	ACA	TTG	ACT	GTA	TTA	720
	<u> </u>	Trp	Ile	Thr	Tyr	Asn	Arg	Leu	Arg	Arg	Asp	Leu	Thr	Leu	Thr	Val	Leu	
	f=1	225					230					235					240	
	in	GAT	ATC	GCC	GCT	TTC	TTT	CCA	AAC	TAT	GAC	AAT	AGG	AGA	TAT	CCA	ATT	768
	rei rei	Asp	Ile	Ala	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile	
	35					245					250					255		
	F=																	
		CAG	CCA	GTT	GGT	CAA	CTA	ACA	AGG	GAA	GTT	TAT	ACG	GAC	CCA	ATT	ATT	816
		Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile	
					260					265					270			
•	40																	
		AAT	TTT	AAT	CCA	CAG	TTA	CAG	TCT	GTA	GCT	CAA	ATT	CCT	ACT	TTT	AAC	864
		Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn	
				275					280					285				
•	45	GTT	ATG	GAG	AGC	AGC	GCA	ATT	AGA	AAT	CCT	CAT	ATT	TTT	GAT	ATA	TTG	912
		Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu	
			290					295					300					
		AAT	AAT	CTT	ACA	ATC	TTT	ACG	GAT	TGG	TTT	AGT	GTT	GGA	CGC	AAT	TTT	960
	50	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe	
		305					310					315					320	

						CGA Arg											1008
5						TAT Tyr											1056
10						GGA Gly											1104
15						CAA Gln											1152
20						GAA Glu 390											1200
20 C C C C C C						GTT Val											1248
25						CGC Arg											1296
30 13						TCT Ser											1344
						CGT Arg											1392
40						ATA Ile 470											1440
70						ACA Thr											1488
45	CGA Arg	AGA Arg	AAT Asn	ACC Thr 500	TTT Phe	GGT Gly	GAT Asp	TTT Phe	GTA Val 505	TCT Ser	CTA Leu	CAA Gln	GTC Val	AAT Asn 510	ATT Ile	AAT Asn	1536
50						AGA Arg											1584

		Ala			Leu			Ser		GTG Val	1632
5								ACT Thr		ATA Ile 560	1680
10								GAT Asp			1728
15								ATA Ile			1776
20								CTT Leu 605			1824
								GCA Ala	 		1872
25								ACT Thr			1920
# 3 0								ATT Ile			1968
								CTG Leu	_		2016
40								CTC Leu 685			2064
70			-					TAA neA			2112
45								CAA Gln			2160
50								ACC Thr		_	2208

				Tyr			Ile			Leu	AAA Lys	2256
5			Arg						Ser		GAC Asp	2304
10		ATC Ile										2352
15		GGC Gly					_					2400
		TGT Cys										2448
		CTA Leu										2496
i.		CAT His 835										2544
		TTA Leu										2592
17 12 85	 -	AGA Arg										2640
40		GCA Ala										2688 -
.0		GAG Glu	-									2736
45		TCT Ser 915										2784
50		GAT Asp										2832

		Arg										Ser				GGT Gly 960	2880
5						Phe					Gly					GCG Ala	2928
10											AAA Lys						2976
15									Lys		CAT His			Val			3024
20			Asn					Leu			CCA Pro		Trp				3072
Grant Alexer Street Control	-	Ser					Val				CGT Arg 1035	Gly					3120
25 						Glu					GGC Gly					His	3168
<u> </u>					Asn					Lys	TTC Phe				Val		3216
55 35				Tyr					Val		TGT Cys			Tyr			3264
40			Glu					Thr			TCT Ser		Asn				3312
.0		Glu					Asn				CCA Pro 1115	Ala					3360
45						Ser					CGA Arg					Суз	3408
50					Gly					Thr	CCA Pro				Gly		3456

GTA ACA AAG GAT TTA GAG-TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile 1155 5 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170 CTC CTT ATG GAG GAA 10 Leu Leu Met Glu Glu Thr Sec ID No:59: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1189 amino acids (B) TYPE: amino acid (C) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID No:59: Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1 5 10 15 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 40 45 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 60 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr 145 150 150 155 160																			
S GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170 1175 CTC CTT ATG GAG GAA Leu Leu Met Glu Glu 1185 (2) INFORMATION FOR SEQ ID NO:59: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1189 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1				Lys	Asp				Phe	Pro				Lys	Val			:	3504
CTC CTT ATG GAG GAA															_				
Leu Leu Met Glu Glu 1185 (2) INFORMATION FOR SEQ ID NO:59: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1189 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQ ID N	5		Ile	Gly				Gly	Thr				Asp	Ser				:	3552
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1189 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: (xi) SEQ ID NO:59: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: (xi) SEQ	10	Leu	Leu															3	3567
(B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1	. 15	(2)									:								
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1											acio	ds							
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1 5 10 15 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 35 40 45 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 60 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr																			
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 45 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	20				(D)	TO	POTO	3Y: 1	linea	ar									
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 45 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	1		(:	ii) M	MOLE	CULE	TYPI	E: pi	rote	in									
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 45 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	. 5							_											
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 45 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	* <u></u> j		()	ci) S	EQUE	ENCE	DESC	CRIPT	CION	SEÇ) ID	NO : 5	59:						
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 35 40 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 Ala Asn Leu Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	125 1-1 1-1		Glu	Glu	Asn		Gln	Asn	Gln	Cys		Pro	Tyr	Asn	Cys		Ser		
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 35		Asn	Pro	Glu	Glu	Val	Leu	Leu	qzA	Gly	Glu	Arq	Ile	Ser	Thr	Gly	Asn		
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 35 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 Ala Asn Leu Glu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	2											,				•			
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr																			
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		Ser	Ser		Asp	Ile	Ser	Leu		Leu	Val	Gln	Phe		Val	Ser	Asn		
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	ij In			35					40					4: 0					
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 70 75 80 40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	· []	Phe	Val	Pro	Gly	Gly	Gly	Phe	Leu	Val	Gly	Leu	Ile	Asp	Phe	Val	Trp		
40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	3 5		50					55			•		60						
40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		<i>a</i>)	T1.		G1	D	C	~1 -	T	3.~~	*1 -	Dha	T 011	V-1	Cln.	Tla	Gl u		
40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr			116	vai	GIA	PIO		GIII	пр	Asp	MIG		neu	Val	GIII	116			
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 110 105 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr																			
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	40	Gln	Leu	Ile	Asn		Arg	Ile	Ala	Glu		Ala	Arg	Asn	Ala		Ile		
Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr					-	85					90					95			
Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		Ala	Asn	Leu	Glu	Glv	Leu	Glv	Asn	Asn	Phe	Asn	Ile	Tyr	Val	Glu	Ala		
Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr								•						•					
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	45					_	_					_			_	_,	_		
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		Phe	Lys		Trp	Glu	Glu	Asp		Asn	Asn	Pro	Ala		Arg	Thr	Arg		
50 130 135 140 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr				TTD					120										
Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		Val	Ile	Asp	Arg	Phe	Arg	Ile	Leu	Asp	Gly	Leu	Leu	Glu	Arg	Asp	Ile		
	50		130					135					140						
		D==	C ^ -	p	71 ~	71 -	c^-	G1 · ·	Dha	G1.1	7751	D~~	ĭ a	T,eu	Cor	Val	Tur		
			ser	rne	ALd	TIE		GTÀ	FILE	GIU	val		neu	neu	Jer	val			

	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170		Arg	Asp	Ser	Val 175	Ile
5	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Cys	Ala	Asn
10	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Ala	Ser 220	Thr	Tyr	Gln	Asp
15	Trp 225	Ile	Thr	Tyr	Asn	Arg 230	Leu	Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
	Asp	Ile	Ala	Ala	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile
20	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265	Val	Tyr	Thr	Asp	Pro 270	Leu	Ile
	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
25 	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
.П ≇ 3•0	Asn 305	Asn	Leu	Thr	Ile	Phe 310	Thr	Asp	Trp	Phe	Ser 315	Val	Gly	Arg	Asn	Phe 320
I I	Tyr	Trp	Gly	Gly	His 325	Arg	Val	Ile	Ser	Ser 330	Leu	Ile	Gly	Gly	Gly 335	Asn
17 35	Ile	Thr	Ser	Pro 340	Ile	Tyr	Gly	Arg	Glu 345	Ala	Asn	Gln	Glu	Pro 350	Pro	Arg
	Ser	Phe	Thr 355	Phe	Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365	Asn	Pro	Thr
40	Leu	Arg 370	Leu	Leu -	Gln	Gln	Pro 375	Trp	Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
45	Gly 385	Val	Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
15	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
50	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys 430	His	Ala
	Thr	Phe	Val 435		Arg	Ser	Gly	Thr	Pro	Phe	Leu	Thr	Thr	Gly	Val	Val

	Phe	Ser 450	-	Thr	His	Arg	Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro
5	Glu 465	_	Ile	Asn	Gln	Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro	Gly	Phe 490	Thr	Gly	Gly	Asp	Ile 495	Leu
10	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln	Val	Asn 510	Ile	Asn
15	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe	Arg	Tyr 525	Ala	Ser	Ser
	Arg	Asp 530	Ala	Arg	Val	Ile	Val 535	Leu	Thr	Gly	Ala	Ala 540	Ser	Thr	Gly	Val
20 []	Gly 545	Gly	Gln	Val	Ser	Val 550	Asn	Met	Pro	Leu	Gln 555	Lys	Thr	Met	Glu	Ile 560
	Gly	Glu	Asn	Leu	Thr 565	Ser	Arg	Thr	Phe	Arg 570	Tyr	Thr	Asp	Phe	Ser 575	Asn
25 La N	Pro	Phe	Ser	Phe 580	Arg	Ala	Asn	Pro	Asp 585	Ile	Ile	Gly	Ile	Ser 590	Glu	Gln
ĻΠ • 3 0	Pro	Leu	Phe 595	Gly	Ala	Gly	Ser	Ile 600	Ser	Ser	Gly	Glu	Leu 605	Tyr	Ile	Asp
	Lys	Ile 610	Glu	Ile	Ile	Leu	Ala 615	Asp	Ala	Thr	Phe	Glu 620	Ala	Glu	Ser	Asp
	Leu 625	Glu	Arg	Ala	Gln	Lys 630	Ala	Val	Asn	Ala	Leu 635	Phe	Thr	Ser	Ser	Asn 640
	Gln	Ile	Gly	Leu	Lys 645	Thr	Asp	Val	Thr	Asp 650	Tyr	His	Ile	Asp	Gln 655	Val
40	Ser	Asn	Leu	Val 660	Asp	Суз	Leu	Ser	Asp 665	Glu	Phe	Cys	Leu	Asp 670	Glu	Lys
45	Arg	Glu	Leu 675	Ser	Glu	Lys	Val	Lys 680	His	Ala	Lys	Arg	Leu 685	Ser	Asp	Glu
	Arg	Asn 690	Leu	Leu	Gln	Asp	Pro 695	Asn	Phe	Arg	Gly	Ile 700	Asn	Arg	Gln	Pro
50	Asp 705	Arg	Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	Asp 720
	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp	Glu

	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745	Ile	Asp	Glu	Ser	Lys 750	Leu	Lys
5	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	Arg 760	Gly	Tyr	Ile	Glu	Asp 765	Ser	Gln	Asp
	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn
10	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800
15	Gly	Lys	Cys	Gly	Glu 805	Pro	Asn	Arg	Суз	Ala 810	Pro	His	Leu	Glu	Trp 815	Asn
	Pro	Asp	Leu	Asp 820	Cys	Ser	Суз	Arg	Asp 825	Gly	Glu	Lys	Cys	Ala 830	His	His
20	Ser	His	His 835	Phe	Thr	Leu	Asp	Ile 840	Asp	Val	Gly	Cys	Thr 845	Asp	Leu	Asn
0	Glu	Asp 850	Leu	Gly	Val	Trp	Val 855	Ile	Phe	Lys	Ile	Lys 860	Thr	Gln	Asp	Gly
25 	His 865	Ala	Arg	Leu	Gly	Asn 870	Leu	Glu	Phe	Leu	Glu 875	Glu	Lys	Pro	Leu	Leu 880
.Л 30	Gly	Glu	Ala	Leu	Ala 885	Arg	Val	Lys	Arg	Ala 890	Glu	Lys	Lys	Trp	Arg 895	Asp
	Lys	Arg	Glu	Lys 900	Leu	Gln	Leu	Glu	Thr 905	Asn	Ile	Val	Tyr	Lys 910	Glu	Ala
<u>[]</u> 35	Lys	Glu	Ser 915	Val	Asp	Ala	Leu	Phe 920	Val	Asn	Ser	Gln	Tyr 925	Asp	Arg	Leu
	Gln	Val 930	Asp	Thr	Asn	Ile	Ala 935	Met	Ile	His	Ala	Ala 940	Asp	Lys	Arg	Val
40	His 945	Arg	Ile	Arg -	Glu	Ala 950	Tyr	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960
45	Val	Asn	Ala	Ala	Ile 965	Phe	Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala
	Tyr	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn
50	Asn	Gly	Leu 995	Leu	Суз	Trp	Asn	Val		Gly	His	Val	Asp 100		Glu	Glu
	Gln	Asn		His	Arg	Ser	Val	Leu 5	Val	Ile	Pro	Glu 102		Glu	Ala	Glu

	Val 102	Ser 5	Gln	Glu	Val	Arg		Cys	Pro	Gly	Arg		Tyr	Ile	Leu	Arg 1040		
5	Val	Thr	Ala	Tyr	Lys 104		Gly	Tyr	Gly	Glu 105		Cys	Val	Thr	Ile 105			
	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 1065		Phe	Ser	Asn	Cys 107		Glu		
10	Glu	Glu	Val 107	_	Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 108		Thr	Gly		
15	Thr	Gln 1090		Glu	Tyr	Glu	Gly 1095		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr		
13	Asp 110	Glu 5	Ala	Tyr	Gly	Asn 1110		Pro	Ser	Val	Pro 1115		Asp	Tyr	Ala	Ser 1120		
20	Val	Tyr	Glu	Glu	Lys 1125		Tyr	Thr	Asp	Gly 1130	_	Arg	Glu	Asn	Pro 1135			
20 11 25	Glu	Ser	Asn	Arg 1140		Tyr	Gly	Asp	Tyr 1145		Pro	Leu	Pro	Ala 1150		Tyr		
25 - 1	Val	Thr	Lys 1155	-	Leu	Glu	Tyr	Phe 1160		Glu	Thr	Asp	Lys 1165		Trp	Ile		
	Glu	Ile 1170	-	Glu	Thr	Glu	Gly 1175		Phe	Ile	Val	Asp 1180		Val	Glu	Leu		
	Leu 1185	Leu 5	Met	Glu	Glu											<u>]~</u>		
3-5	(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10 : 60):									
40		(i)	(P (E	QUENC A) LE B) TY C) SI O) TO	NGTH PE: RANI	nucl	67 b eic ESS:	ase ació sing	pair I	s								
45			(<i>I</i>	ATURE A) NA B) LO	ME/F	ON:	13											
				QUENC												3 am	4.0	
50		GAG Glu															4.8	,

				Val				_			Gly	AAT Asn	96	
5					CTG Leu				_				144	
10					TTT Phe 55								192	
. 15					CAA Gln								240	
2 0					ATA Ìle								288	
Here Mare Lord Hall					GGA Gly							-	336	
25 \ []					GAT Asp								384	
					ATA Ile 135								432	
11 13 35					GGA Gly								480	
40	_	_	 Ala		CAT His	_	_				_		528	
			-		TTG Leu								576	
45					ATT Ile					_	-		624	
50					AAT Asn 215								672	

	Ile				Leu			Thr		Leu 240	720
5		GCC Ala		Phe			Asn				768
10		GTT Val									816
15		AAT Asn 275									86 4
20		GAG Glu									912
Tree from the first		CTT Leu									960
25 *.; !!!		GGA Gly									1008
		TCT Ser			_						1056
35		ACT Thr 355									1104
40		TTA Leu									1152
		G AA Glu	-								1200
45	 	AGA Arg									1248
50		GTG Val									1296

				Gln				Pro			Gly		GTA Val	1344
5			Trp							Thr			CCA Pro	1392
10		Arg	ATT Ile											1440
15			TCT Ser											1488
20			AAT Asn											1536
20 0 0 1			ATT Ile 515											1584
			GCA Ala			Ile								1632
30 T			CAA Gln		Ser							Glu		1680
[] [35			AAC Asn					Phe						1728
40			TCA Ser											1776
		Leu	TTT Phe 595	_			Ser				Tyr			1824
45	Lys		GAA Glu			Leu								1872
50			AGA Arg											1920

	_	_		Thr			Tyr			GTA Val	1968
5				TGT Cys							2016
10	_			AAA Lys							2064
15				GAT Asp		_					2112
20		_		GGA Gly 710							2160
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1				AAT Asn							2208
25 				TTA Leu							2256
10				GAA Glu							2304
				ATC Ile							2352
40				TCC Ser 790							2400
.0			-	CCG Pro							2448
45				TCC Ser							2496
50				TTG Leu							2544

		Leu								Thr		GGC Gly	2592
5									Glu			TTA Leu 880	2640
10										AAG Lys			2688
15										TAT Tyr			2736
20										TAT Tyr 925			2784
										GAT Asp			2832
25 H 1										GTG Val			2880
30										ATT Ile			2928
										GGC Gly			2976
40							Lys			GAT Asp 1005	Val		3024
.0		Asn	-			Leu				TGG Trp			3072
45	Ser				Val				Gly	TAT Tyr			3120
50				Glu				Gly		GTA Val		His	3168

					Asn					AAA Lys 5					Val		3216
5				Tyr					Val	ACG Thr				Tyr			3264
10			Glu					Thr		ACT Thr			Asn				3312
. 15		Glu					Asn			GTA Val		Ala					3360
20						Ser				GGA Gly 1130	Arg					Cys	3408
20 					Gly					ACA Thr					Gly		3456
25 				Asp					Pro	GAG Glu				Val			3504
30			Gly					Thr		ATC Ile			Ser				3552
		Leu	ATG Met														3567
	(2)	INF	ORMA!	NOIT	FOR	SEQ	ID N	10 : 6 1	L:								
40			(i) s	(A) (B)	LEN TY		: 118 amino	39 am o aci	nino id	: acio	ls						
45		(ii) 1	MOLE	CULE	TYPE	E: pi	rote	in								
										Q ID							
50	Met 1	Glu	Glu	Asn	Asn 5	Gln	Asn	Gln	СЛа	Ile 10	Pro	Tyr	Asn	Суз	Leu 15	Ser	
	Asn	Pro	Glu	Glu 20		Leu	Leu	Asp	Gly 25		Arg	Ile	Ser	Thr 30		Asn	

	Ser	Ser	35	Asp	IIe	Ser	Leu	Ser 40	Leu	vai	GIII	FILE	45	vai	Ser	ASI
5	Phe	Val 50	Pro	Gly	Gly	Gly	Phe 55	Leu	Val	Gly	Leu	Ile 60	Asp	Phe	Val	Trp
	Gly 65	Ile	Val	Gly	Pro	Ser 70	Gln	Trp	Asp	Ala	Phe 75	Leu	Val	Gln	Ile	Glu 80
10	Gln	Leu	Ile	Asn	Glu 85	Arg	Ile	Ala	Glu	Phe 90	Ala	Arg	Asn	Ala	Ala 95	Ile
15	Ala	Asn	Leu	Glu 100	Gly	Leu	Gly	Asn	Asn 105	Phe	Asn	Ile	Tyr	Val 110	Glu	Ala
	Phe	Lys	Glu 115	Trp	Glu	Glu	Asp	Pro 120	Asn	Asn	Pro	Ala	Thr 125	Arg	Thr	Arg
2 0	Val	Ile 130	Asp	Arg	Phe	Arg	Ile 135	Leu	Asp	Gly	Leu	Leu 140	Glu	Arg	Asp	Ile
2 0	Pro 145	Ser	Phe	Asp	Ile	Ser 150	Gly	Phe	Glu	Val	Pro 155	Leu	Leu	Ser	Val	Tyr 160
2 -5 √ ∏	Ala	Gln	Ala	Ala	Asn 165	Leu	His	Leu	Ala	Ile 170	Leu	Arg	Asp	Ser	Val 175	Ile
<u>-</u> 30	Phe	Gly	Glu	Arg 180	Trp	Gly	Leu	Thr	Thr 185	Ile	Asn	Val	Asn	Glu 190	Asn	Tyr
	Asn	Arg	Leu 195	Ile	Arg	His	Ile	Asp 200	Glu	Tyr	Ala	Asp	His 205	Cys	Ala	Asn
35	Thr	Tyr 210	Asn	Arg	Gly	Leu	Asn 215	Asn	Leu	Pro	Ala	Ser 220	Thr	Tyr	Gln	Asp
	Trp 225	Ile	Thr	Tyr	Asn	Arg 230		Arg	Arg	Asp	Leu 235	Thr	Leu	Thr	Val	Leu 240
40	Asp	Ile	Ala	Ala -	Phe 245	Phe	Pro	Asn	Tyr	Asp 250	Asn	Arg	Arg	Tyr	Pro 255	Ile
45	Gln	Pro	Val	Gly 260	Gln	Leu	Thr	Arg	Glu 265	Val	Tyr	Thr	Asp	Pro 270	Leu	Ile
	Asn	Phe	Asn 275	Pro	Gln	Leu	Gln	Ser 280	Val	Ala	Gln	Leu	Pro 285	Thr	Phe	Asn
50	Val	Met 290	Glu	Ser	Ser	Ala	Ile 295	Arg	Asn	Pro	His	Leu 300	Phe	Asp	Ile	Leu
	Asn		Leu	Thr	Ile	Phe		Asp	Trp	Phe	Ser 315		Gly	Arg	Asn	Phe 320

	Ty	r Trj	o Gly	/ Gly	/ His		y.Va]	l Ile	e Ser	330		ı Ile	e Gly	/ Gly	/ Gly 335	/ Asn
5	Ile	ì Thi	. Ser	Pro 340		Tyr	Gly	/ Arg	Glu 345		Asn	Gln	. Glu	9rc 350		Arg
	Ser	Phe	355		Asn	Gly	Pro	Val 360	Phe	Arg	Thr	Leu	Ser 365		Pro	Thr
10	Leu	Arg 370		Leu	Gln	Gln	Pro 375		Pro	Ala	Pro	Pro 380	Phe	Asn	Leu	Arg
15	Gly 385		Glu	Gly	Val	Glu 390	Phe	Ser	Thr	Pro	Thr 395	Asn	Ser	Phe	Thr	Tyr 400
	Arg	Gly	Arg	Gly	Thr 405	Val	Asp	Ser	Leu	Thr 410	Glu	Leu	Pro	Pro	Glu 415	Asp
20	Asn	Ser	Val	Pro 420	Pro	Arg	Glu	Gly	Tyr 425	Ser	His	Arg	Leu	Cys 430	His	Ala
	Thr	Phe	Val 435	Gln	Arg	Ser	Gly	Thr 440	Pro	Phe	Leu	Thr	Thr 445	Gly	Val	Val
25 \	Phe	Ser 450	Trp	Thr	His	Arg	Ser 455	Ala	Thr	Leu	Thr	Asn 460	Thr	Ile	Asp	Pro
30	Glu 465	Arg	Ile	Asn	Gln	Ile 470	Pro	Leu	Val	Lys	Gly 475	Phe	Arg	Val	Trp	Gly 480
	Gly	Thr	Ser	Val	Ile 485	Thr	Gly	Pro		Phe 490	Thr	Gly	Gly		Ile 495	Leu ~
35	Arg	Arg	Asn	Thr 500	Phe	Gly	Asp	Phe	Val 505	Ser	Leu	Gln		Asn 510	Ile	Asn
	Ser	Pro	Ile 515	Thr	Gln	Arg	Tyr	Arg 520	Leu	Arg	Phe		Tyr 525	Ala	Ser	Ser
40	Arg	Asp 530	Ala	Arg	Val	Ile	Val 535	Leu	Thr	Gly	Ala .	Ala 540	Ser	Thr	Gly	Val
45	Gly 545	Gly	Gln	Val	Ser	Val 550	Asn	Met	Pro		Gln 555	Lys	Thr	Met	Glu	Ile 560
	Gly	Glu	Asn		Thr 565	Ser	Arg	Thr		Arg 570	Tyr	Thr .	Asp		Ser 575	Asn
50	Pro	Phe		Phe 580	Arg	Ala	Asn	Pro	Asp 585	Ile	Ile	Gly		Ser 590	Glu	Gln
	Pro		Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly		Leu	Tyr	Ile	Asp

	Ly	/s I: 6:	le Gl 10	u Il	e Il	e Le	u Al 61		p Al	a Th	ır Ph	e Gl 62		.a G	lu Se	er Asp
5	Le 62	u G]	lu Ar	g Al	a Gl	n Ly:		a Va	l As	n Al	a Le 63		e Th	r Se	er Se	er Asn 640
	Gl	n Il	e Gl	y Le	u Ly:	s Thi	r As	p Va	l Th	r As _i		r Hi	s Il	e As	p G1 65	n Val 5
10	Se	r As	n Lei	u Va:	l Asp	Cys	Lei	ı Sei	Asp 665		u Phe	e Cys	s Le	u As 67		u Lys
15	Arg	g Gl	u Lei 675	ı Ser	Glu	Lys	Va]	Lys 680	His	Ala	ı Lys	arg	685		r Ası	o Glu
	Arg	690	n Leu O	ı Leu	Gln	Asp	Pro 695	Asn	Phe	Arg	g Gly	700		Arg	g Glr	ı Pro
20	Asp 705	Arg	g Gly	Trp	Arg	Gly 710	Ser	Thr	Asp	Ile	Thr 715	Ile	Gln	Gly	Gly	720
1	Asp	Val	. Phe	Lys	Glu 725	Asn	Tyr	Val	Thr	Leu 730	Pro	Gly	Thr	Val	Asp 735	
25	Cys	Tyr	Pro	Thr 740	Tyr	Leu	Tyr	Gln	Lys 745	Ile	Asp	Glu	Ser	Lys 750	Leu	Lys
3 <u>0</u>	Ala	Tyr	Thr 755	Arg	Tyr	Glu	Leu	Arg 760	Gly	Tyr	Ile	Glu	Asp 765	Ser	Gln	Asp
T T	Leu	Glu 770	Ile	Tyr	Leu	Ile	Arg 775	Tyr	Asn	Ala	Lys	His 780	Glu	Ile	Val	Asn
() 35	Val 785	Pro	Gly	Thr	Gly	Ser 790	Leu	Trp	Pro	Leu	Ser 795	Ala	Gln	Ser	Pro	Ile 800
	Gly	Lys	Суз	Gly	Glu 805	Pro	Asn	Arg		Ala 810	Pro	His	Leu	Glu	Trp 815	Asn
40	Pro	Asp	Leu	Asp 820	Суз	Ser	Cys	Arg	Asp 825	Gly	Glu	Lys	Cys	Ala 830	His	His
45	Ser	His	His 835	Phe	Thr	Leu	Asp	Ile 840	Asp	Val	Gly	Cys	Thr 845	Asp	Leu	Asn
	Glu	Asp 850	Leu	Gly	Val		Val 855	Ile	Phe	Lys		Lys 860	Thr	Gln	Asp	Gly
50	His 865	Ala	Arg	Leu		Asn : 870	Leu	Glu	Phe		Glu 875	Glu	Lys	Pro	Leu	Leu 880
	Gly	Glu	Ala	Leu	Ala 885	Arg '	Val	Lys		Ala 890	Glu	Lys	Lys		Arg 895	Asp

	D, S	ALG	, GIU	900		GII	, nec	GIU	905		. 116	val	. iyi	910		. Ala
5	Lys	Glu	Ser 915		Asp	Ala	Leu	Phe 920		Asn	Ser	Gln	Tyr 925	_	Arg	Leu
	Gln	Val 930	Asp	Thr	Asn	Ile	Ala 935		Ile	His	Ala	Ala 940	Asp	Lys	Arg	Val
10	His 945	Arg	Ile	Arg	Glu	Ala 950	Tyr	Leu	Pro	Glu	Leu 955	Ser	Val	Ile	Pro	Gly 960
15	Val	Asn	Ala	Ala	Ile 965	Phe	Glu	Glu	Leu	Glu 970	Gly	Arg	Ile	Phe	Thr 975	Ala
	Tyr	Ser	Leu	Tyr 980	Asp	Ala	Arg	Asn	Val 985	Ile	Lys	Asn	Gly	Asp 990	Phe	Asn
20 (3	Asn	Gly	Leu 995	Leu	Суз	Trp	Asn	Val 1000		Gly	His	Val	Asp 1009		Glu	Glu
	Gln	Asn 1010	Asn)	His	Arg	Ser	Val 1019		Val	Ile	Pro	Glu 1020		Glu	Ala	Glu
25) 	Val 1025		Gln	Glu	Val	Arg 1030		Cys	Pro	Gly	Arg 1035		Tyr	Ile	Leu	Arg 1040
3 0	Val	Thr	Ala	Tyr	Lys 1045		Gly	Tyr	Gly	Glu 1050	-	Cys	Val	Thr	Ile 1055	
j	Glu	Ile	Glu	Asp 1060		Thr	Asp	Glu	Leu 1065	-	Phe	Ser	Asn	Cys 1070		Glu
3 5 3	Glu	Glu	Val 1075		Pro	Asn	Asn	Thr 1080		Thr	Cys	Asn	Asn 1085	_	Thr	Gly
	Thr	Gln 1090	Glu	Glu	Tyr	Glu	Gly 1095		Tyr	Thr	Ser	Arg 1100		Gln	Gly	Tyr
40	Asp 1105		Ala	Tyr -	Gly	Asn 1110		Pro	Ser	Val	Pro 1115		Asp	Tyr	Ala	Ser 1120
45	Val	Tyr	Glu	Glu	Lys 1125		Tyr	Thr	Asp	Gly 1130		Arg	Glu	Asn	Pro 1135	
	Glu	Ser	Asn	Arg 1140		Tyr	Gly	Asp	Tyr 1145		Pro	Leu	Pro	Ala 1150		Tyr
50	Val	Thr	Lys 1155	, -	Leu	Glu	Tyr	Phe 1160		Glu	Thr	Asp	Lys 1169		Trp	Ile
	Glu	Ile 1170	Gly	Glu	Thr	Glu	Gly 1175		Phe	Ile	Val	Asp 1180		Val	Glu	Leu

Leu Leu Met Glu Glu 1185

5	(2) INFORMATION FOR SEQ ID NO:62:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 47 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
15	CGGGGATTAA ATAATTTACC GGCTAGCACG TATCAAGATT GGATAAC	47
	(2) INFORMATION FOR SEQ ID NO:63:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 45 base pairs	
ū	(B) TYPE: nucleic acid	
Ō	(C) STRANDEDNESS: single	
୍ଧୁ ଜ	(D) TOPOLOGY: linear	
0 0 25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	CGGGGATTAA ATAATTTACC GAAAAACGTA TCAAGATTGG ATAAC	45
	(2) INFORMATION FOR SEQ ID NO:64:	
# 22 1	(i) SEQUENCE CHARACTERISTICS:	
IJ	(A) LENGTH: 23 base pairs	
55	(B) TYPE: nucleic acid	
ł d	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
70	GGATAGCACT CATCAAAGGT ACC	23
	(2) INFORMATION FOR SEQ ID NO:65:	
45		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 45 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single	
<i>5</i> 0	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
	CGGGGATTAA ATAATACCGA AAAGCACGTA TCAAGATTGG ATAAC	45

	(2) INFORMATION FOR SEQ ID NO:66:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
	CGGGGATTAA ATAATTTAAA AAAGCACGTA TCAAGATTGG ATAAC	45
15	(2) INFORMATION FOR SEQ ID NO:67:	
20 10 10 10 10 10 10 10 10 10 10 10 10 10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
25 ≒ [∏	CGGGGATTAA ATAATTTACC GAAGCACGTA TCAAGATTGG ATAAC	45
50 C C C C C C C C C C C C C C C C C C C	(2) INFORMATION FOR SEQ ID NO:68: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
33	(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
40	GGATTAAATA ATTTACCGAA AAGCATATCA AGATTGGATA ACATATAATC G	51
	(2) INFORMATION FOR SEQ ID NO:69:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
	GGATTAAATA ATTTACCGAA AAGCACGACA AGATTGGATA ACATATAATC G	51

	(2) INFORMATION FOR SEQ ID NO:70:	•
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70: GATTCTGTAA TTTTTAGAAA GATGGGGATT GACAACGATA AATGTCAATG	50
	GATTETGTAA TITTTAGAAA GATGGGGGATT GACAACGATA AATGTCAATG	30
15	(2) INFORMATION FOR SEQ ID NO:71:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 50 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
210	(D) TOPOLOGY: linear	
₩ .n	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
* <u>* * * * * * * * * * * * * * * * * * </u>	(XI) SEQUENCE DESCRIPTION. SEQ ID NO:/I:	
20 july 11 25	GATTCTGTAA TTTTTGGAAA GATGGGGATT GACAACGATA AATGTCAATG	50
A THE STATE OF THE	(2) INFORMATION FOR SEQ ID NO:72:	
e I-	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 50 base pairs	
	(B) TYPE: nucleic acid	
M	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
39 5 35	(E)	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
	GATTCTGTAA TTTTTGGAGA AATGGGGGATT GACAACGATA AATGTCAATG	50
40	(2) INFORMATION FOR SEQ ID NO:73:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 52 base pairs	
45	(B) TYPE: nucleic acid	
43	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
50	TCTGTAATTT TTGGAGAAAG AAGGATTGAC AACGATAAAT GTCAATGAAA AC	52
	(2) INFORMATION FOR SEQ ID NO:74:	

	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
10	GTAATTTTTG GAGAAAGATG GATTGACAAC GATAAATGTC AATGAAAAC	49
	(2) INFORMATION FOR SEQ ID NO:75:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 49 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20 □	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
20 급 고 고	GTAATTTTTG GAGAAAGATG GGGAAACAAC GATAAATGTC AATGAAAAC	49
25	(2) INFORMATION FOR SEQ ID NO:76:	
14 14	(i) SEQUENCE CHARACTERISTICS:	
M	(A) LENGTH: 49 base pairs	
£	(B) TYPE: nucleic acid	
3D	(C) STRANDEDNESS: single	
j	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
<u> </u>	GTAATTTTTG GAGAAAGATG GGGATTGAAC GATAAATGTC AATGAAAAC	49